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Godwin et al.

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- (54) **PRIMER EXTENSION TARGET ENRICHMENT**
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(51) **Int. Cl.**

C12Q 1/68 (2018.01)
C12Q 1/6869 (2018.01)
C12Q 1/6806 (2018.01)
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(52) **U.S. Cl.**

CPC **C12Q 1/6869** (2013.01); **C12Q 1/6806** (2013.01); **C12Q 1/6853** (2013.01)

(58) **Field of Classification Search**

None
See application file for complete search history.

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(57) **ABSTRACT**

Improved methods and compositions are provided herein for primer extension target enrichment of target polynucleotides.

5 Claims, 14 Drawing Sheets

Specification includes a Sequence Listing.

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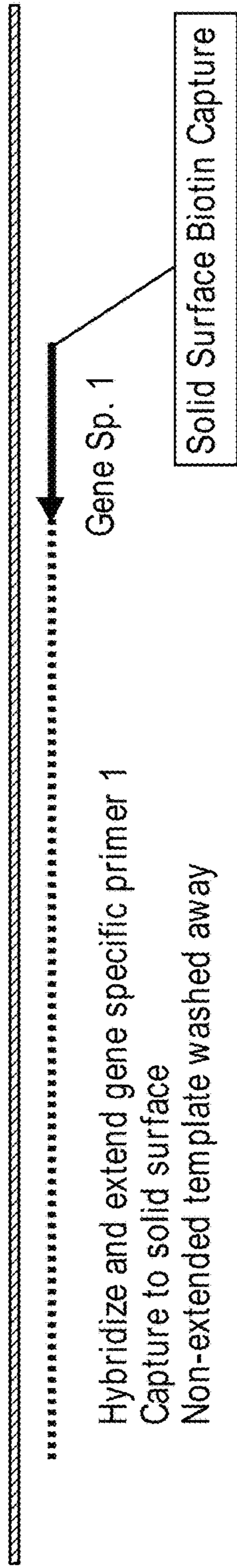


FIG. 1A

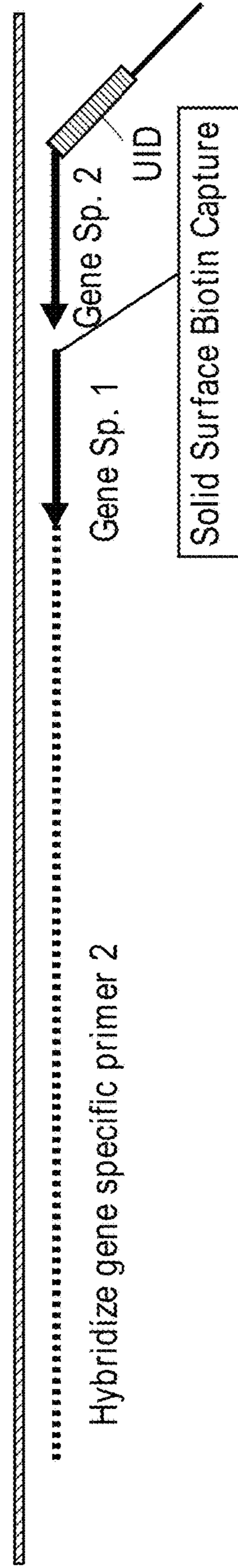


FIG. 1B

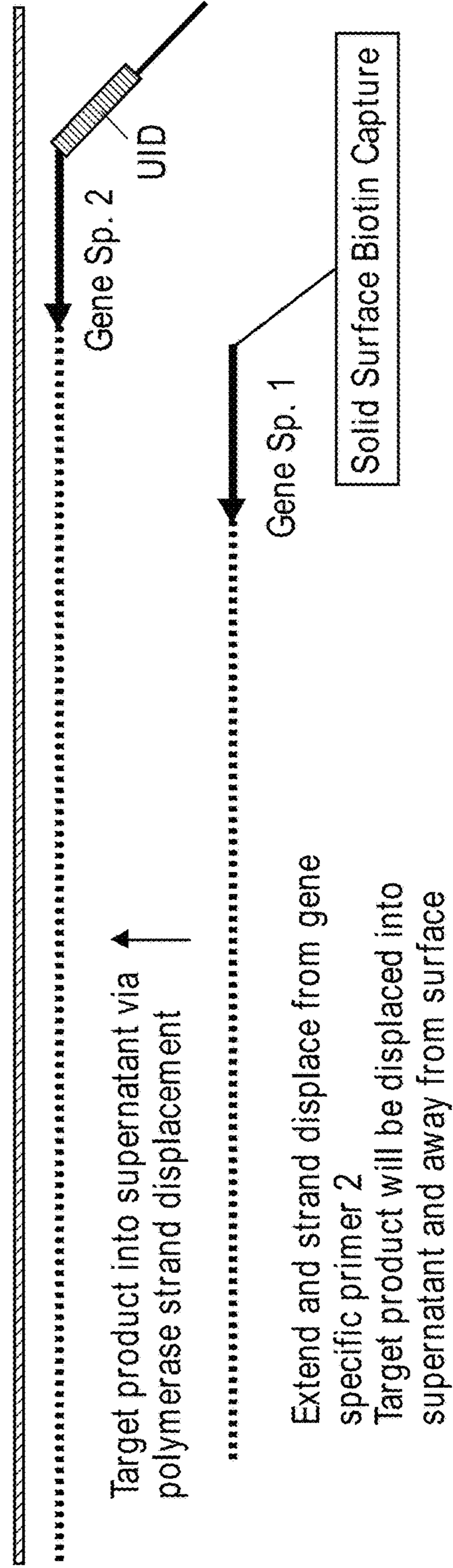
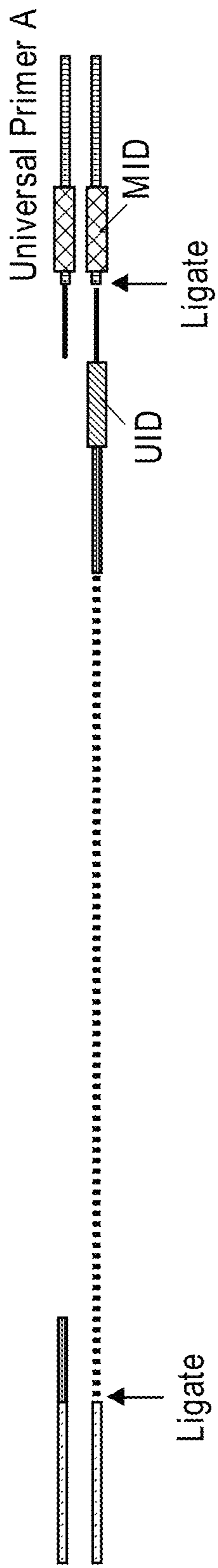
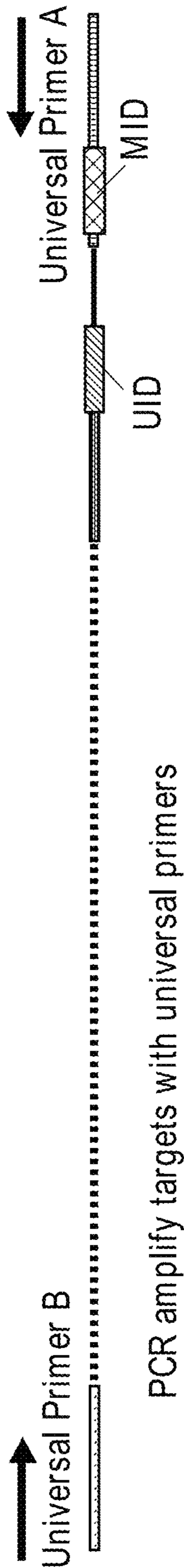


FIG. 1C



Ligate universal adapters to ends of target

FIG. 1D



PCR amplify targets with universal primers

FIG. 1E

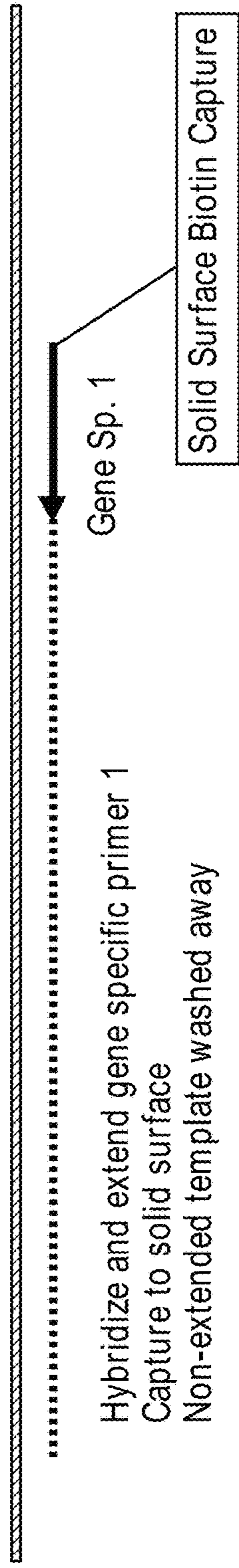


FIG. 2A

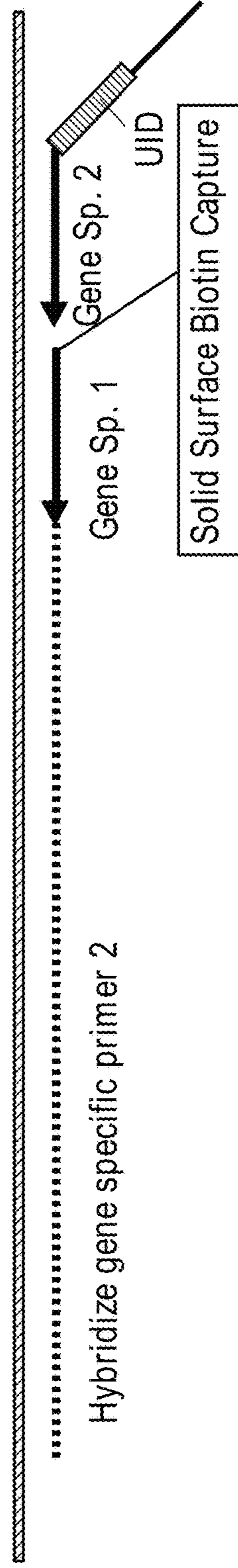


FIG. 2B

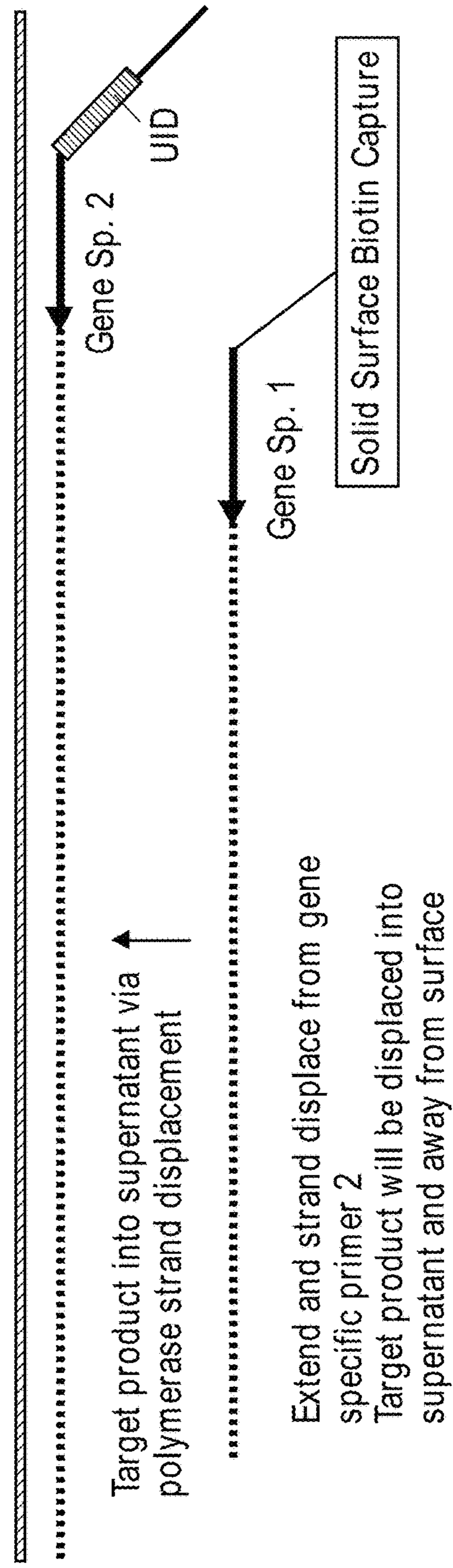


FIG. 2C

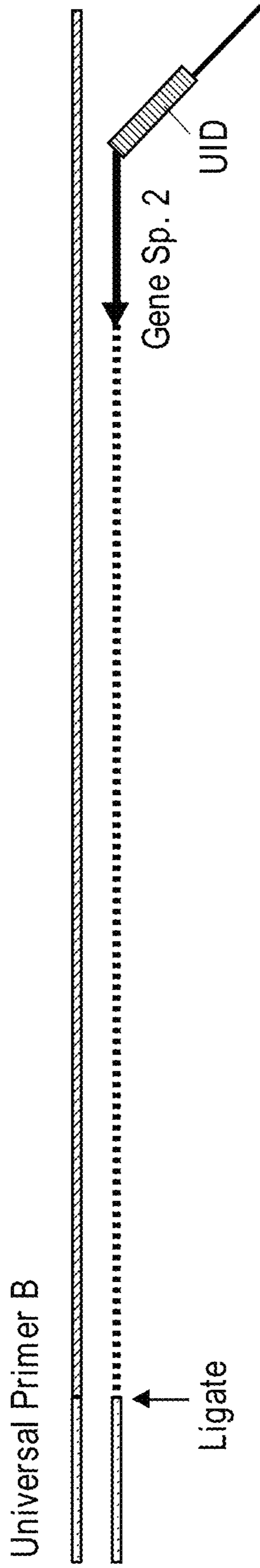


FIG. 2D

Ligate (T4 ligase) universal primer B to dsDNA end; blunt or TA depending on polymerase used for previous extension

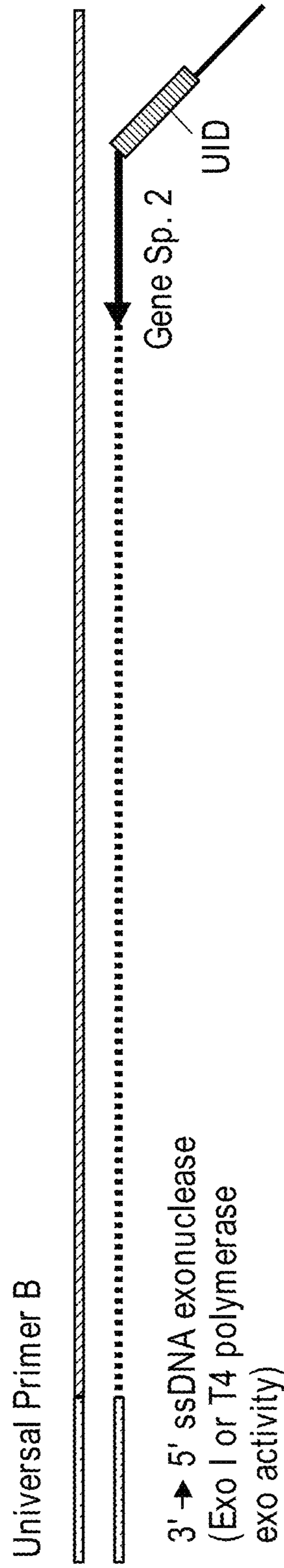


FIG. 2E

3' → 5' ssDNA exonuclease (Exo I or T4 polymerase exo activity)

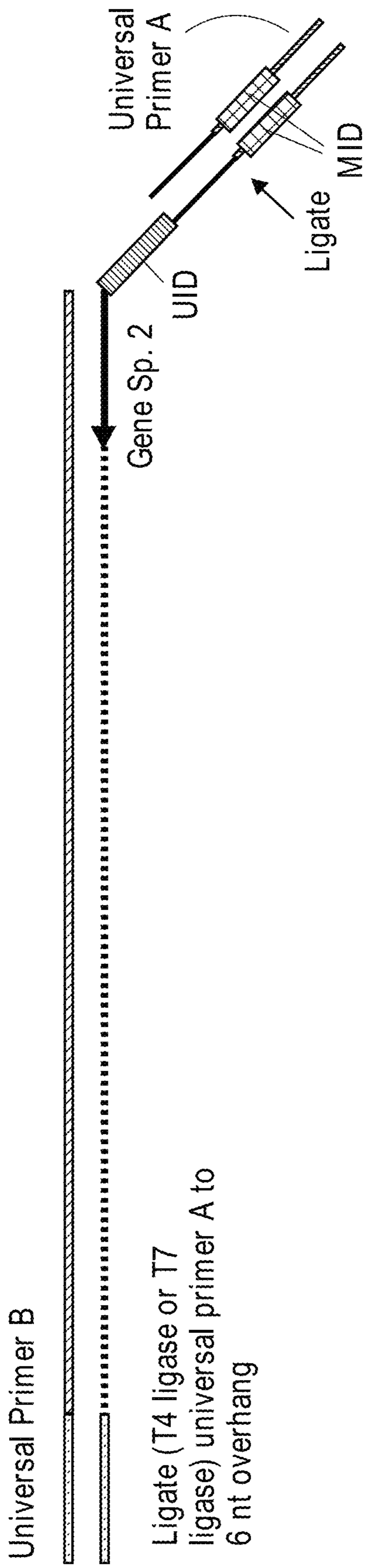


FIG. 3A

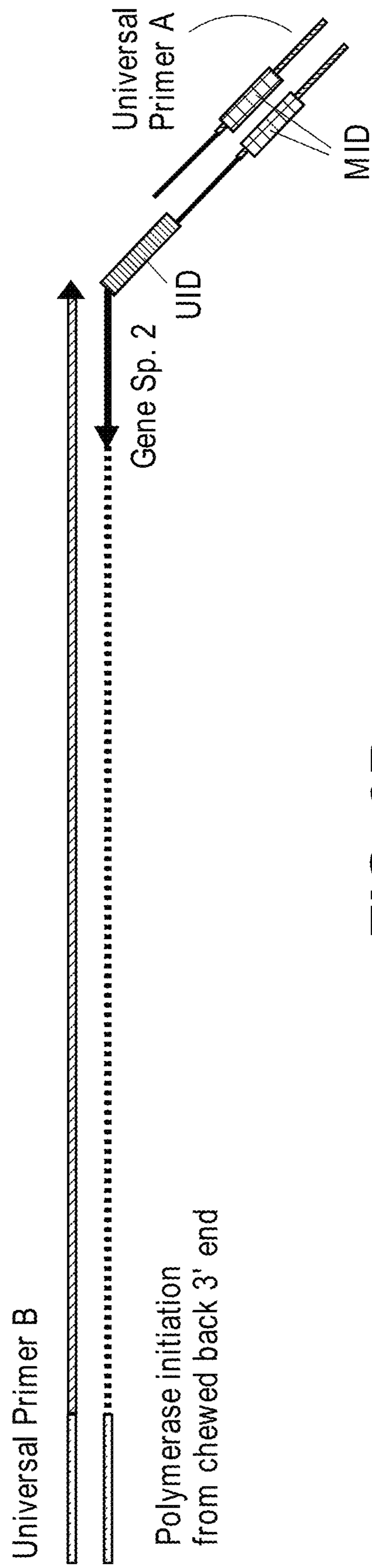


FIG. 3B

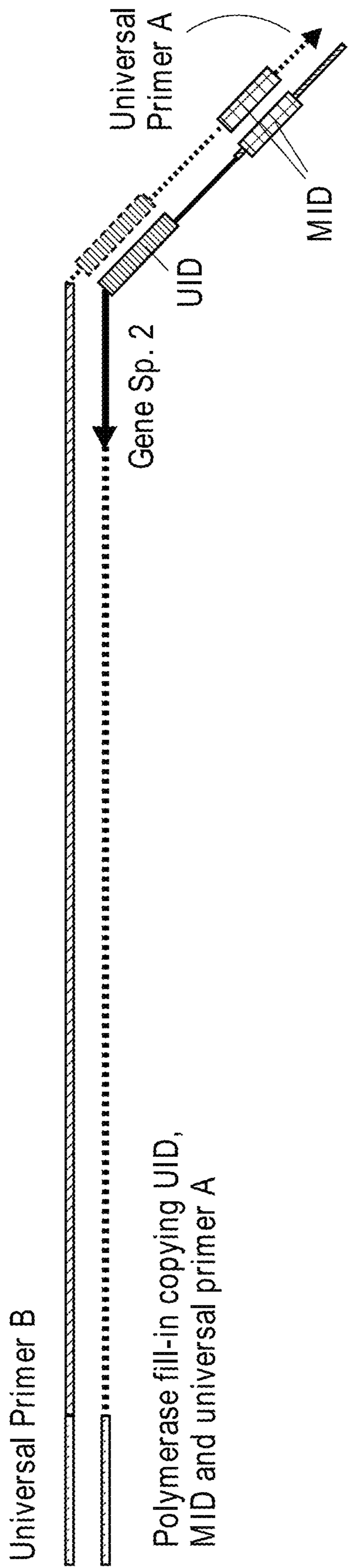


FIG. 3C

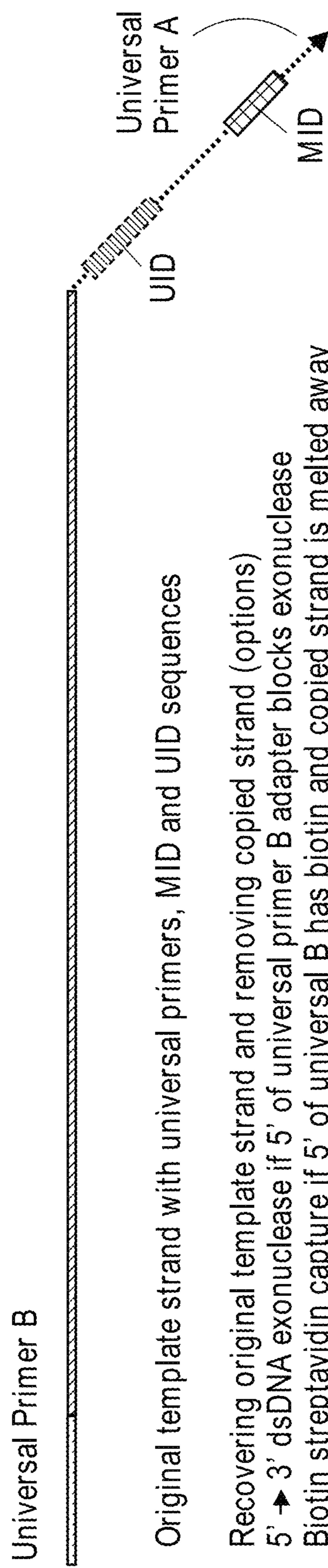


FIG. 3D

Recovering original template strand and removing copied strand (options)
 5' → 3' dsDNA exonuclease if 5' of universal primer B adapter blocks exonuclease
 Biotin streptavidin capture if 5' of universal B has biotin and copied strand is melted away
 Biotin streptavidin capture if 5' of universal A has biotin and original template strand is melted and retained

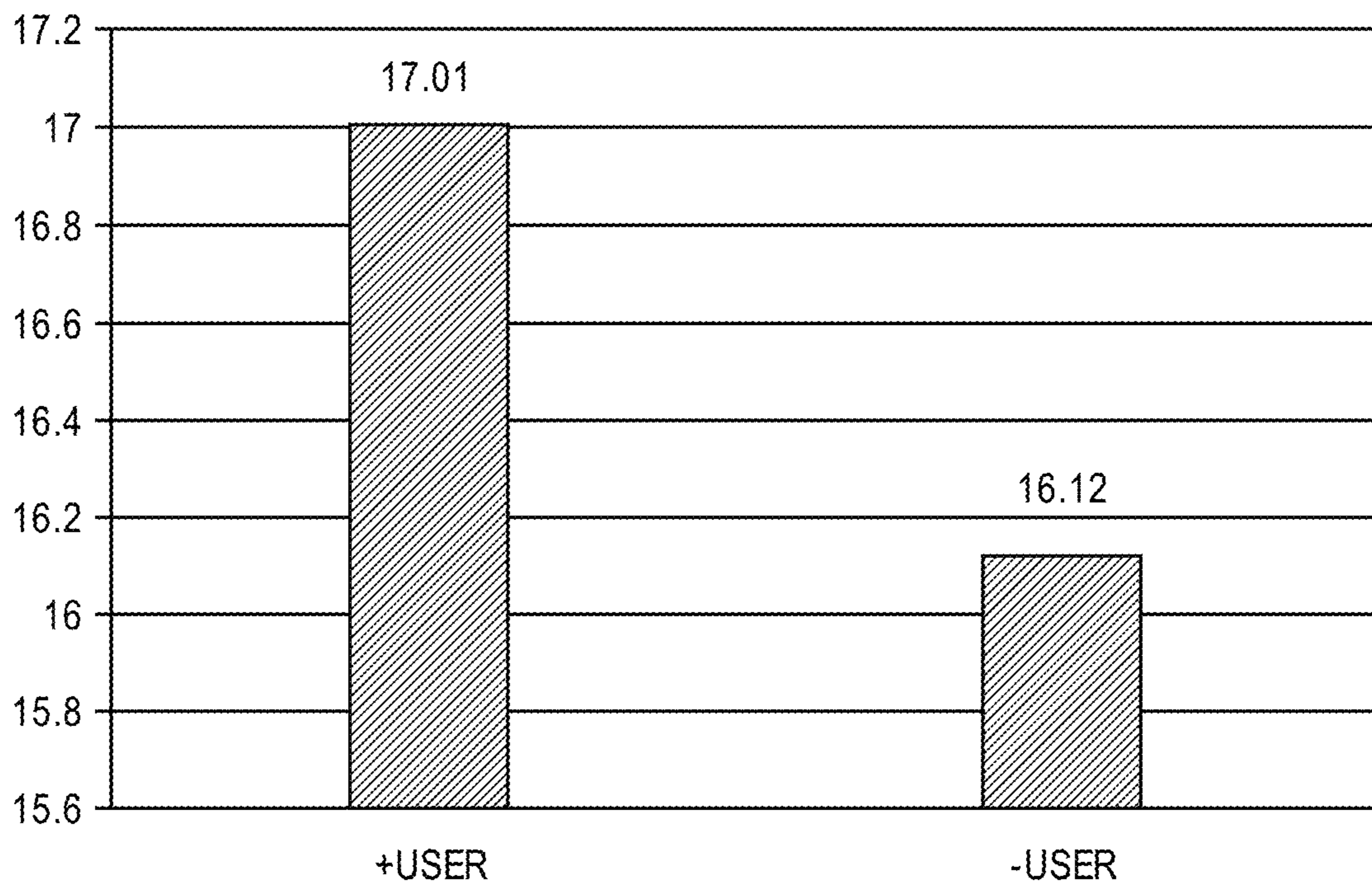


FIG. 4

Double Primer Extension Endonuclease/Full Hybridization

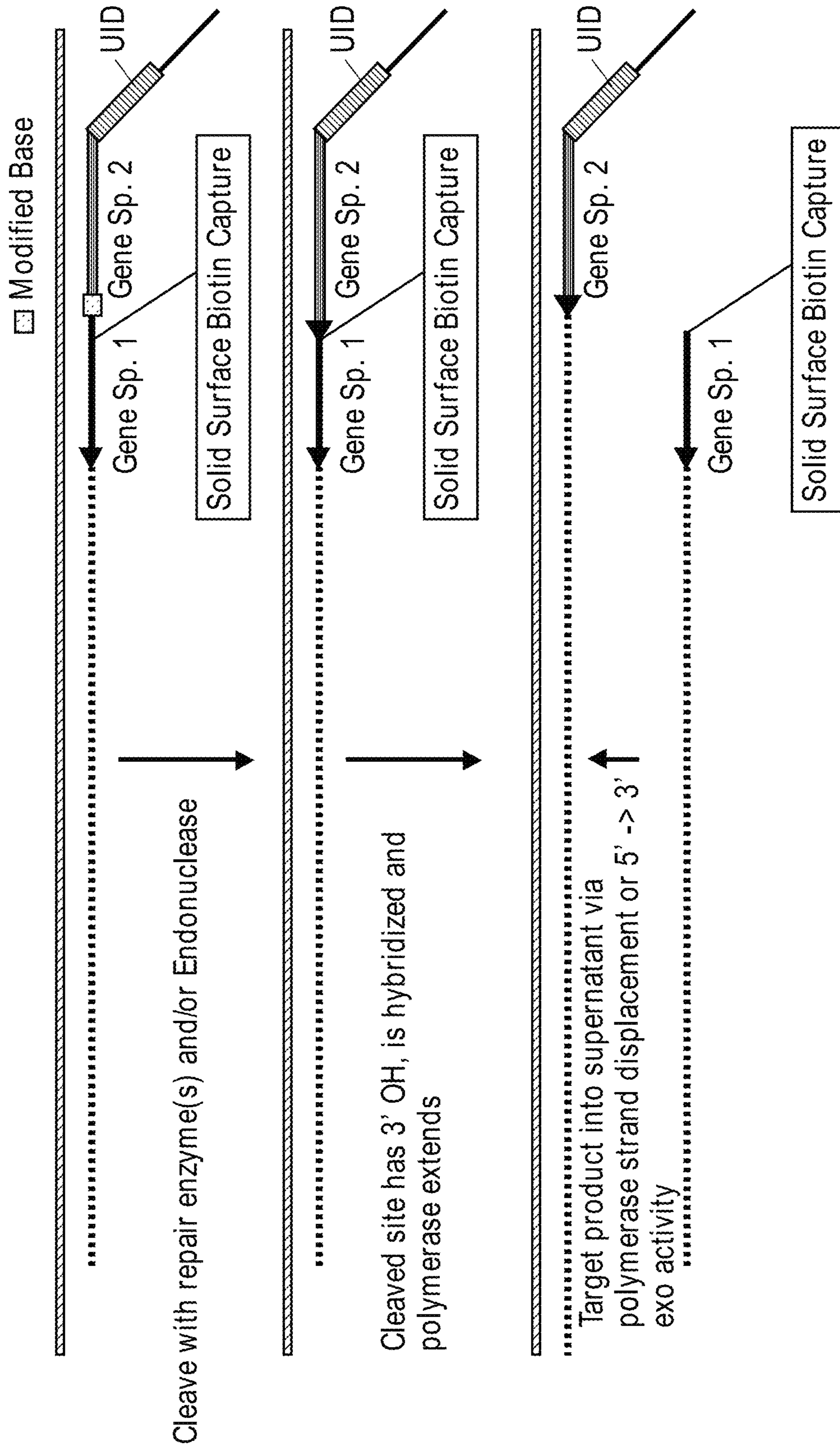


FIG. 5

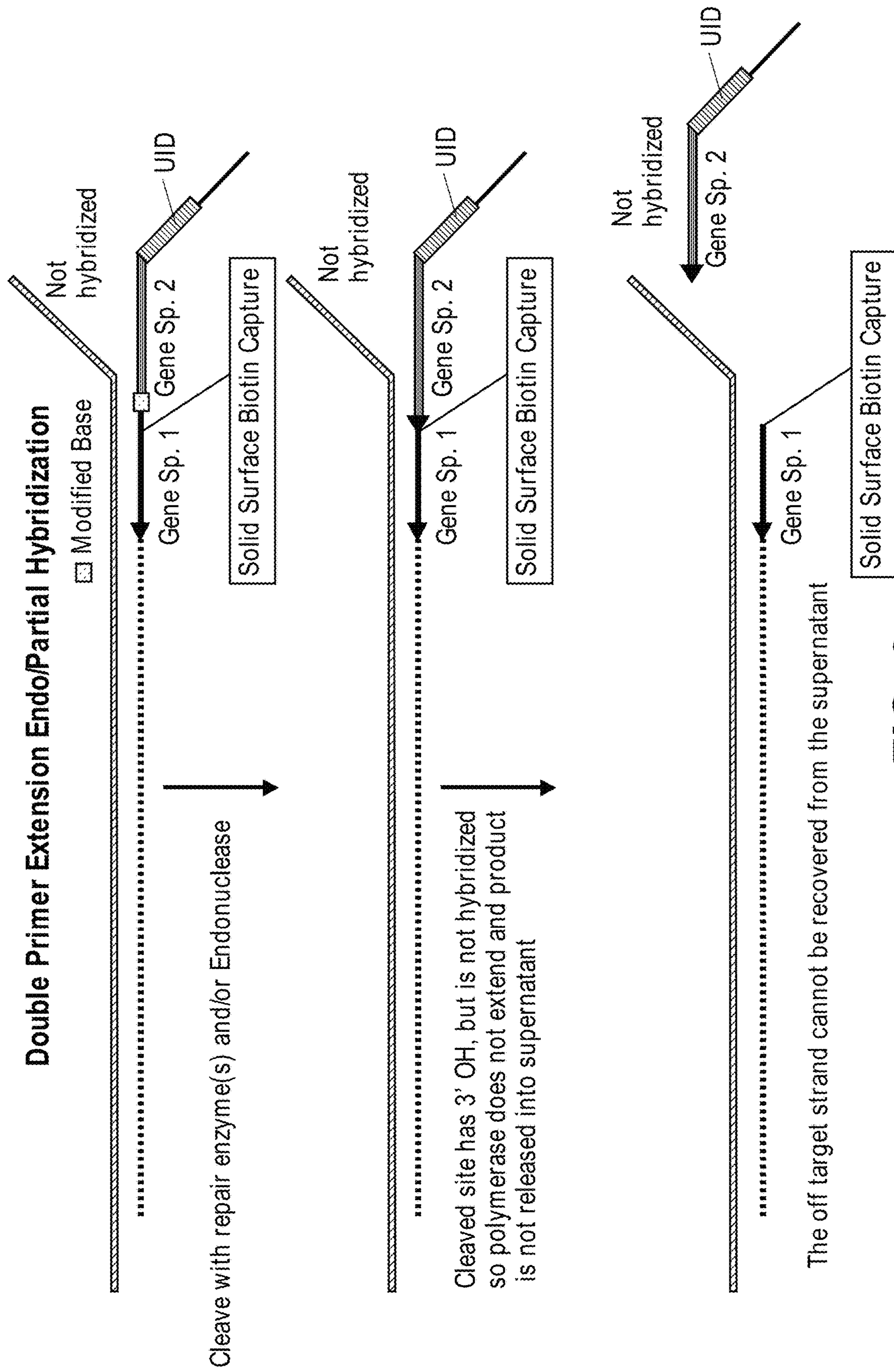


FIG. 6

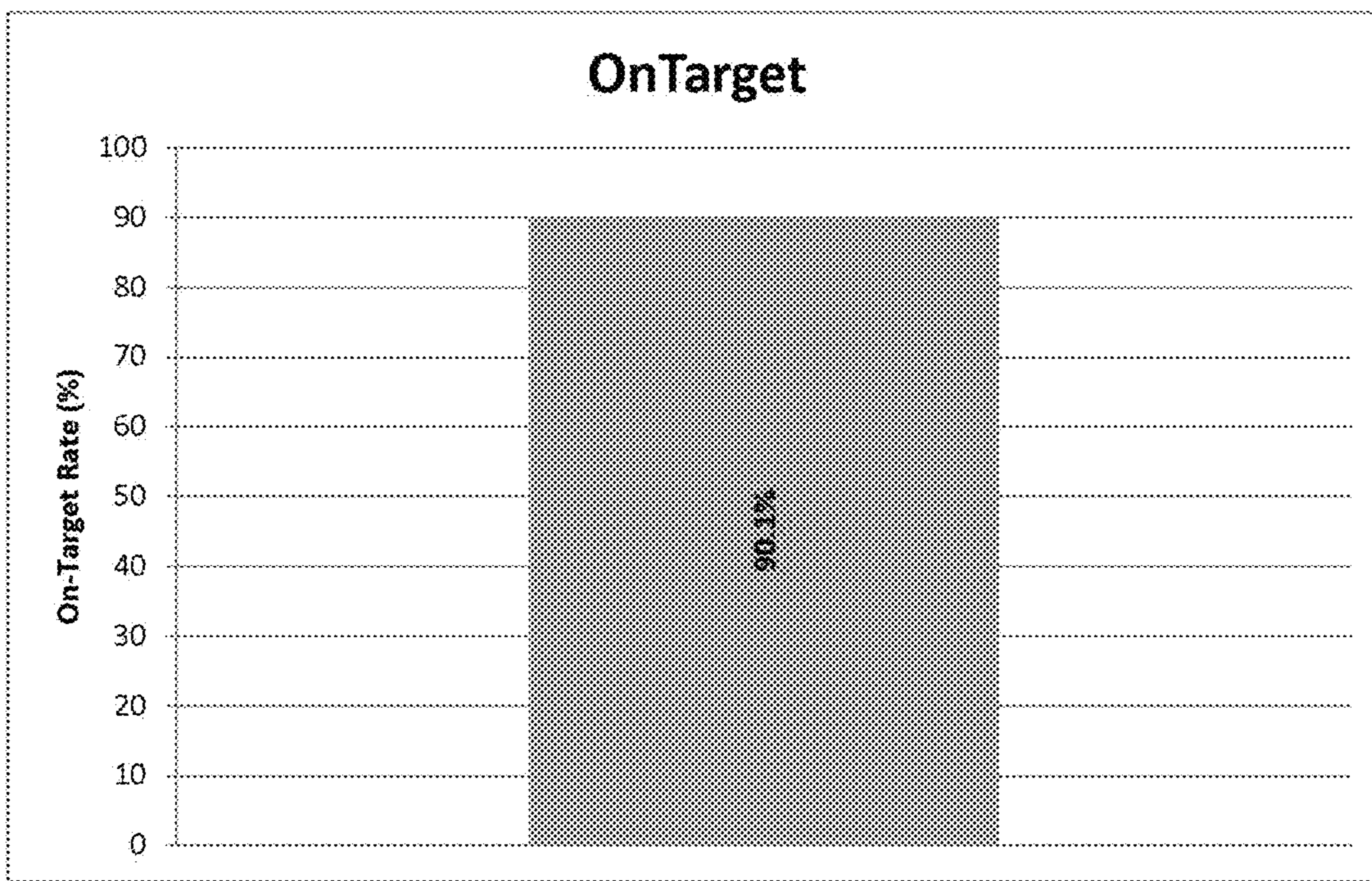


FIG. 7A

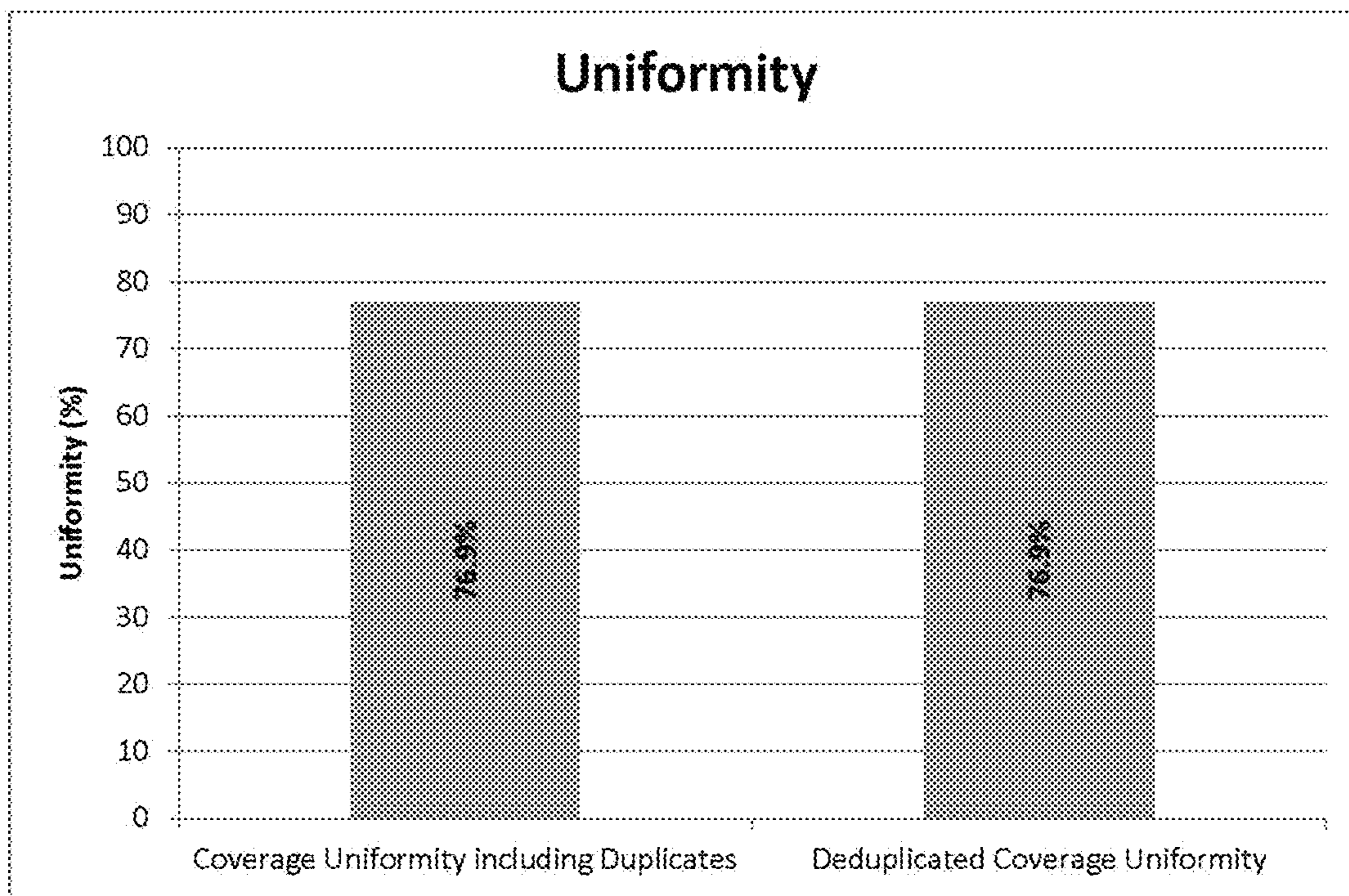


FIG. 7B

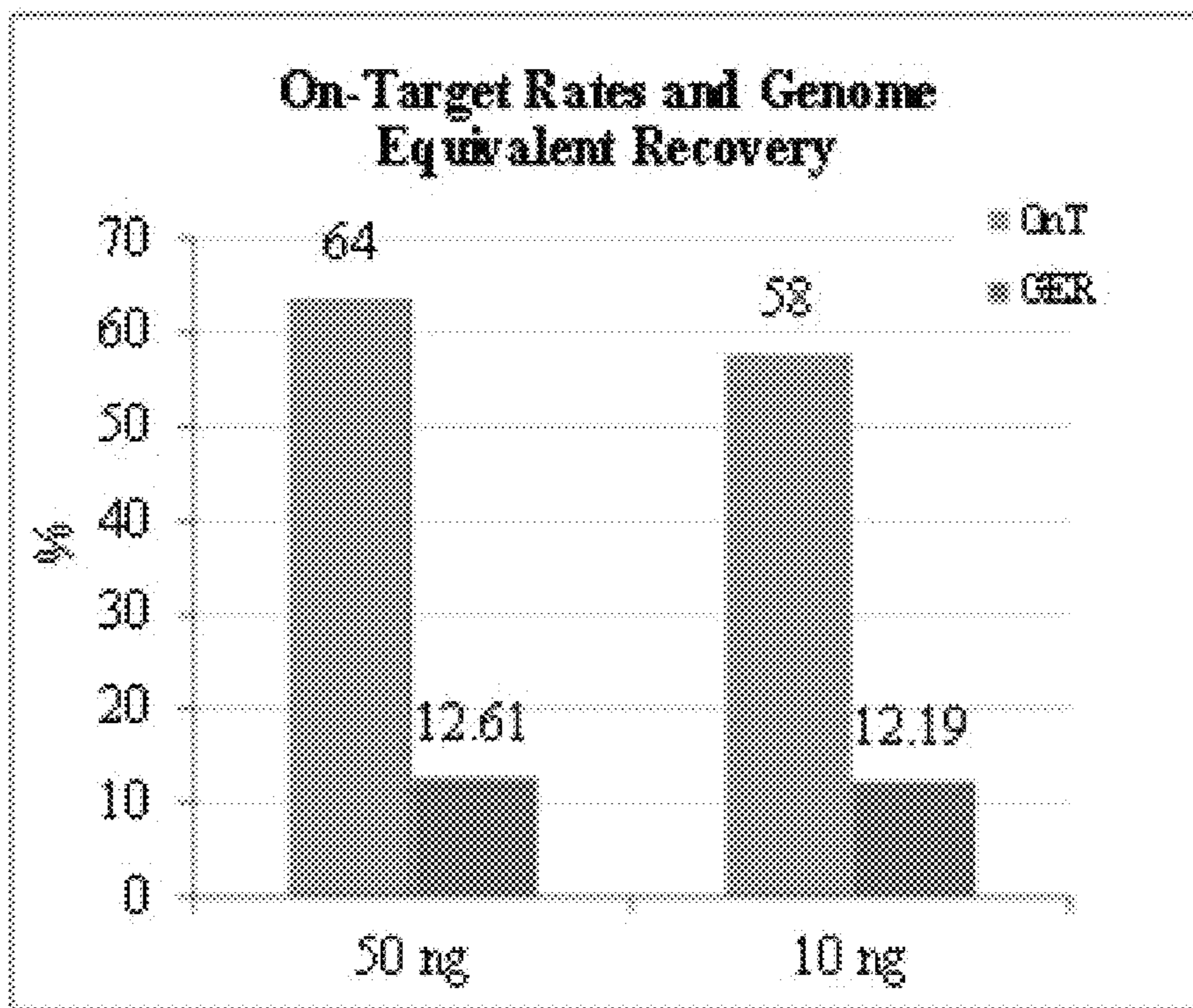


FIG. 8A

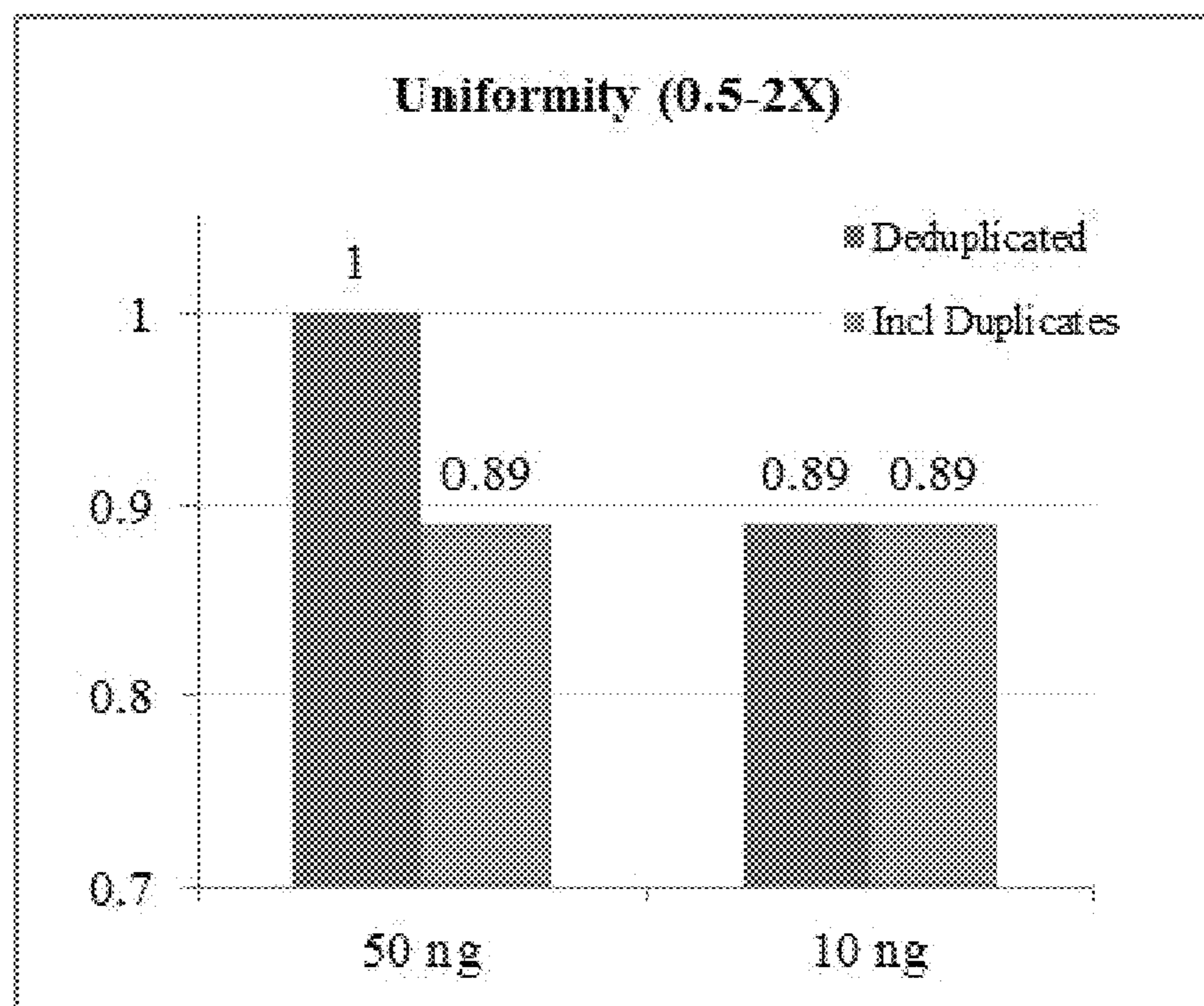


FIG. 8B

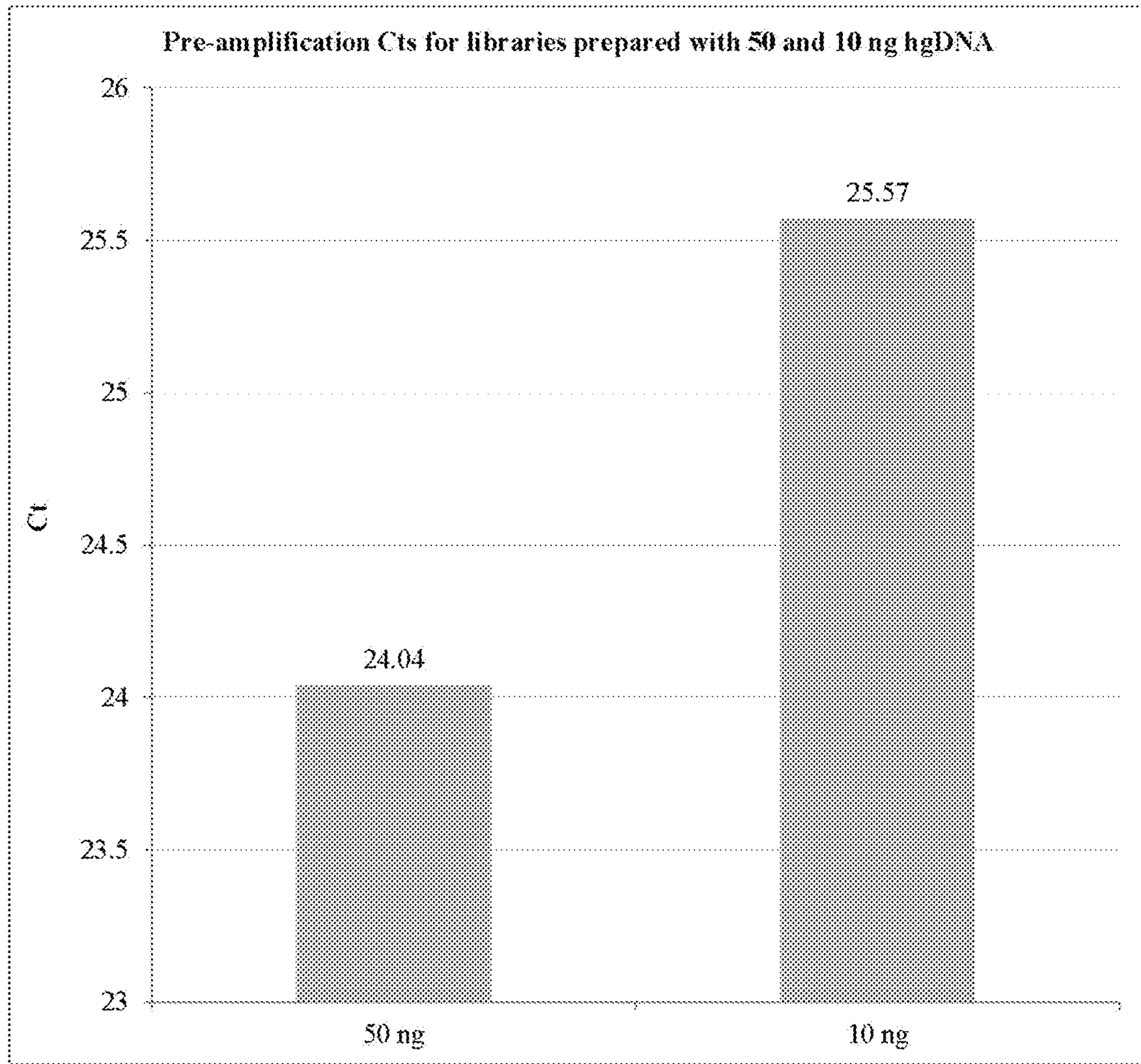


FIG. 9

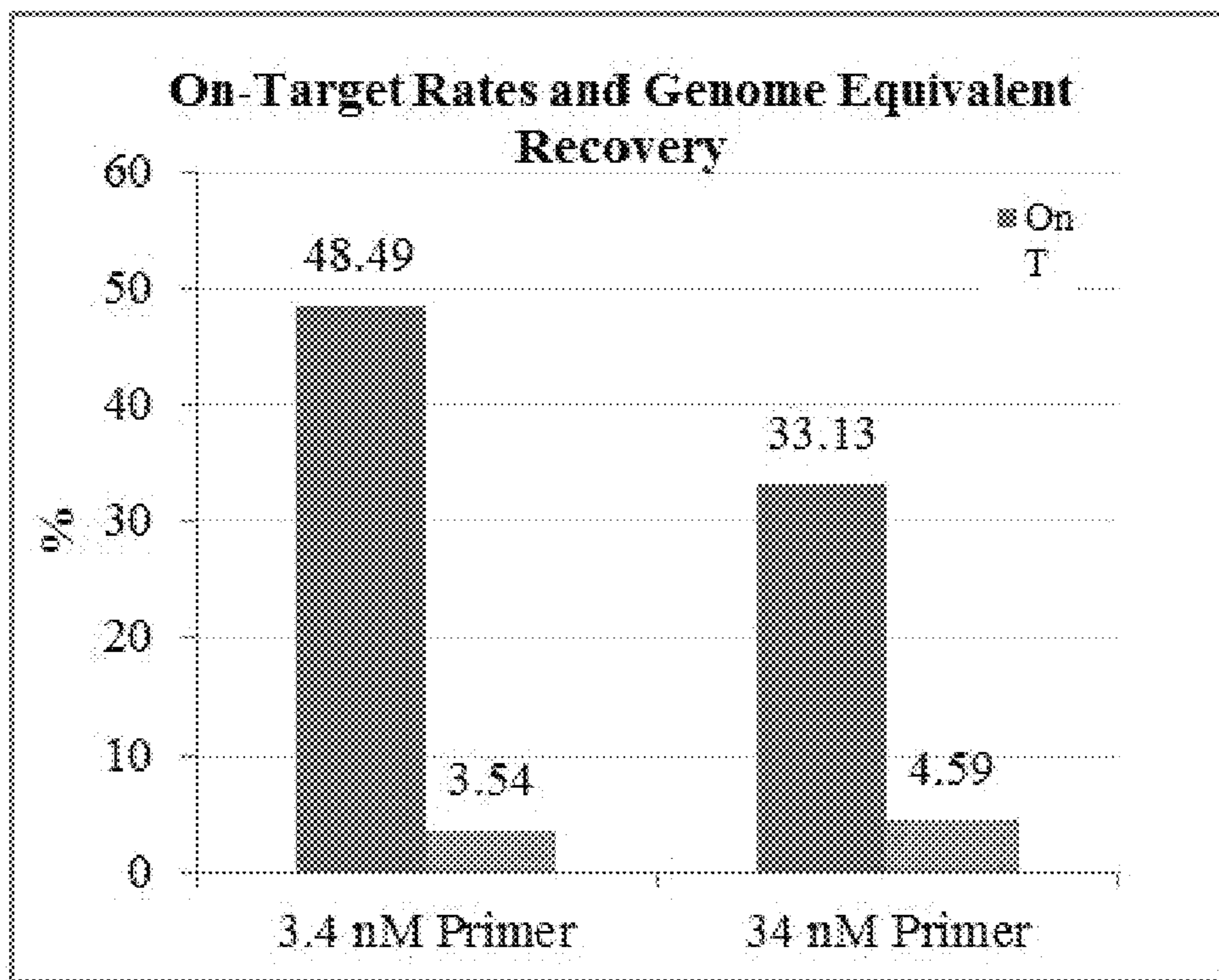


FIG. 10A

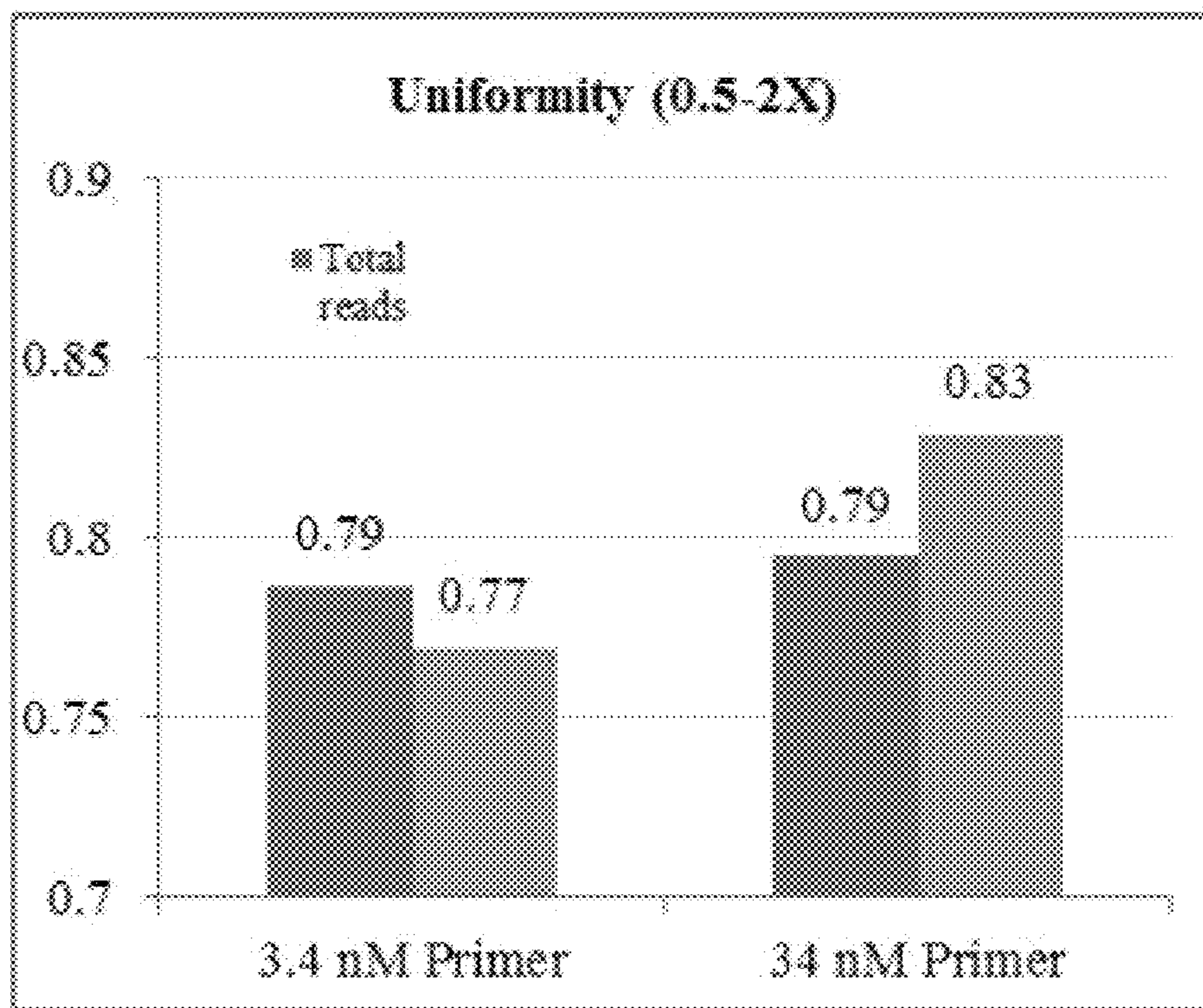


FIG. 10B

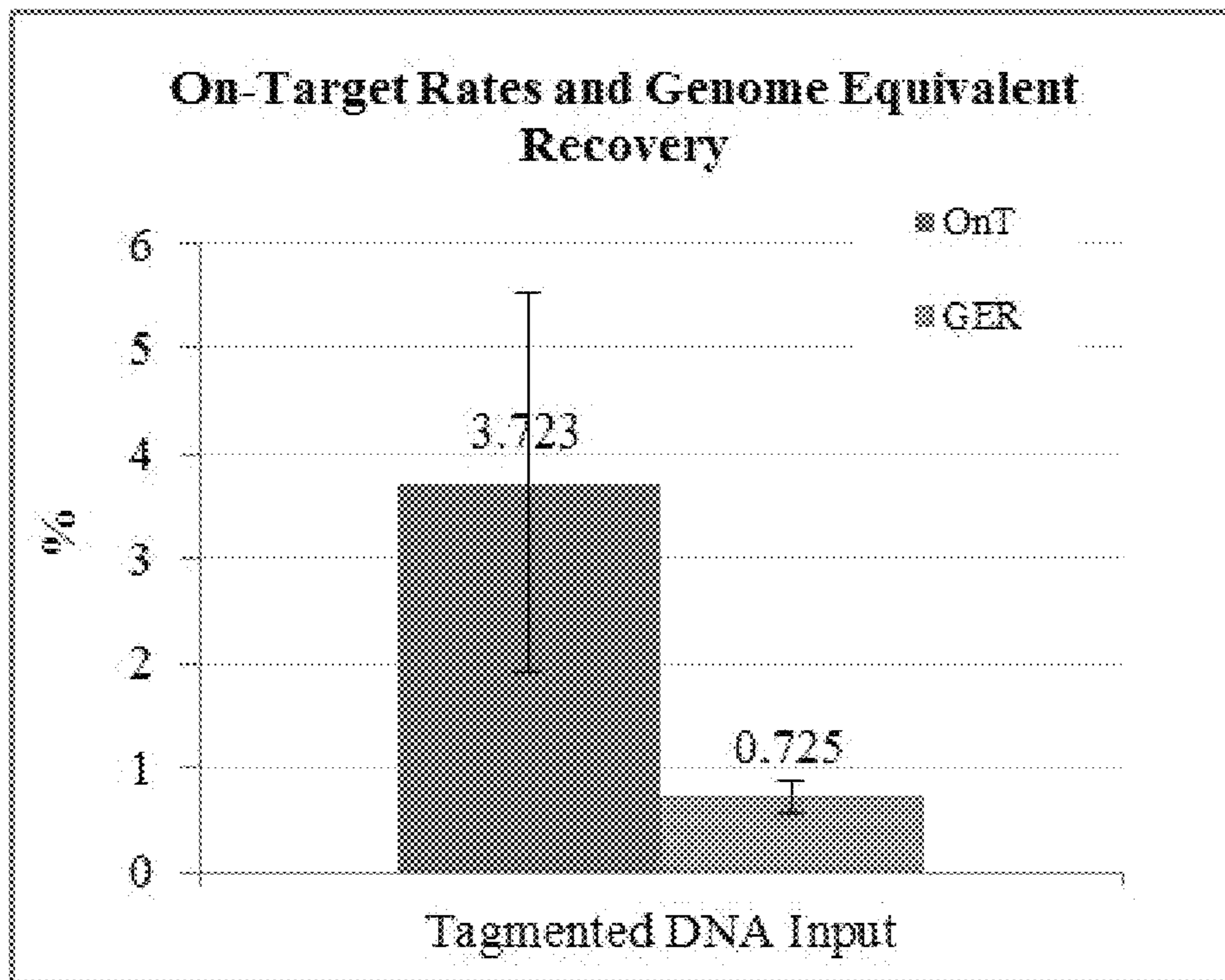


FIG. 11A

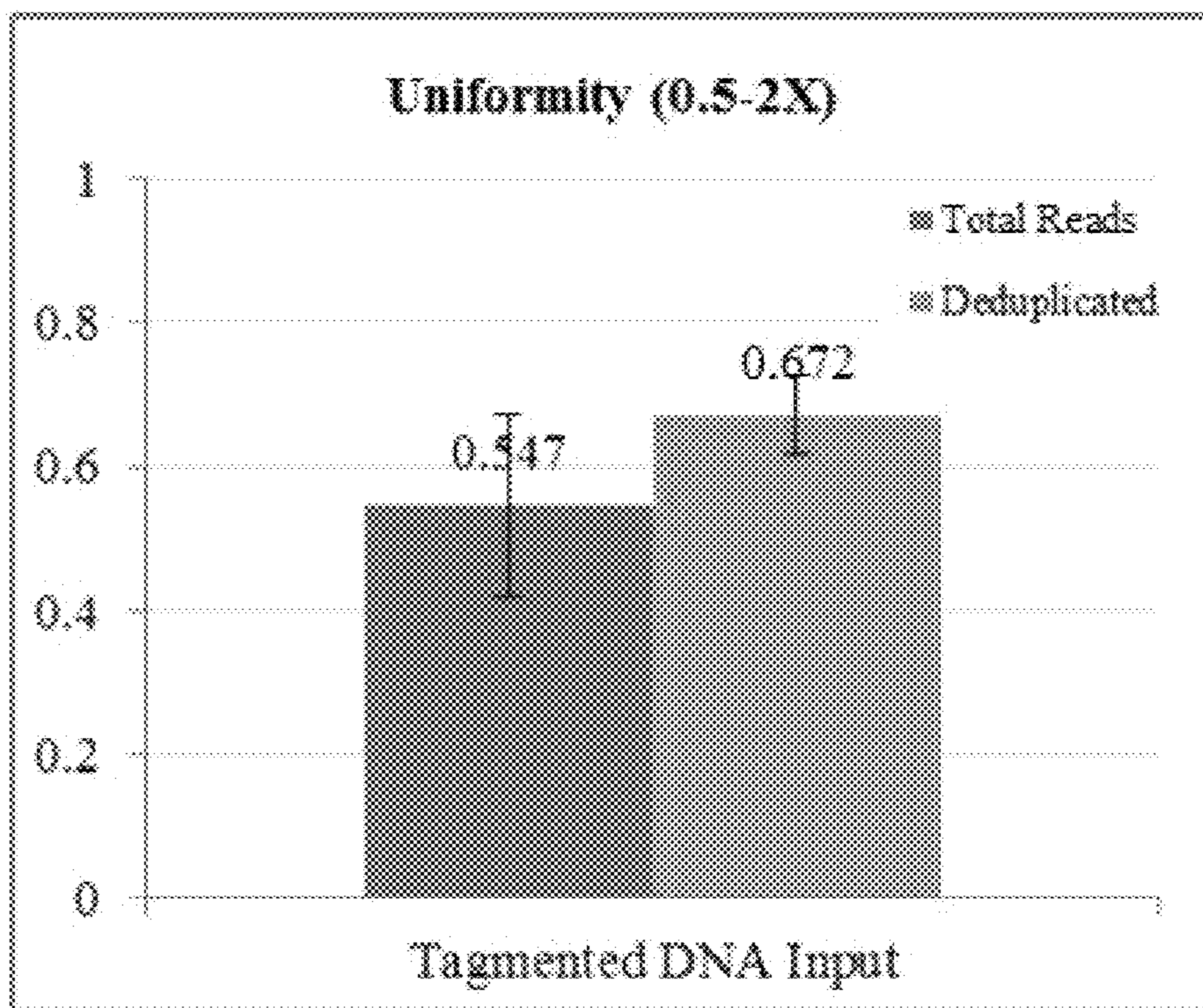


FIG. 11B

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PRIMER EXTENSION TARGET ENRICHMENT

CROSS-REFERENCE TO RELATED PATENT APPLICATIONS

The present application claims benefit of priority to U.S. Provisional Patent Application No. 62/361,426, filed Jul. 12, 2016 and U.S. Provisional Patent Application No. 62/469,480, filed Mar. 9, 2017, each of which are incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

Sample preparation for high-throughput sequencing typically involves an enrichment step that increases the ratio of target nucleic acids to non-target nucleic acids in a sample. Such enrichment can utilize a number of different physicochemical attributes of the target and non-target nucleic acids. See, Mamanova et al., Nat. Methods, 7:111-118 (2010). For example, target nucleic acids having known sequence attributes can be enriched by selecting from a sample nucleic acid fragments having the target sequences. Sequence-based enrichment techniques known in the art include but are not limited to hybrid capture, multiplex PCR amplification, primer extension target enrichment (PETE), linear array, and bead based methods.

BRIEF SUMMARY OF THE INVENTION

Described herein are improved methods and compositions for primer extension target enrichment (PETE) of target nucleic acids from a sample. Methods and compositions described herein can, e.g., be used for preparation of samples for analysis by high-throughput sequencing. In some cases, the methods and compositions described herein can provide increased sensitivity, decreased background, or increased efficiency in high-throughput sequencing library preparation or analysis. In some cases, the improvement is provided by the use of two unidirectional primers that are sequentially hybridized to the same target polynucleotide and extended with a polymerase.

In some embodiments, a method for enriching a target polynucleotide from a sample is provided, the method comprising: providing a reaction mixture comprising the sample and a first target-specific primer, wherein the sample comprises single-stranded target polynucleotide having a 3' and a 5' end and a plurality of structurally different single-stranded non-target polynucleotides; hybridizing a first target-specific primer to the single-stranded target polynucleotide in the reaction mixture, wherein the first target-specific primer hybridizes at least 6 nucleotides from the 3' end of the single-stranded target polynucleotide; extending the hybridized first target-specific primer with a DNA polymerase to form a first double-stranded product comprising the target polynucleotide hybridized to the extended first target-specific primer, wherein the hybridized target polynucleotide comprises a single-stranded overhang region of at least 6 consecutive nucleotides at the 3' end; removing single-stranded target and non-target polynucleotides that are not hybridized to extended target-specific primer, if present from the reaction mixture; hybridizing a second target-specific primer to the single-stranded overhang region at the 3' end of the hybridized target polynucleotide, wherein the second target-specific primer comprises a 3' hybridizing region and a barcode region; and extending the hybridized second target-specific primer with a DNA polymerase,

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wherein the DNA polymerase comprises strand displacement activity, 5'-3' double stranded DNA exonuclease activity, or a combination thereof, thereby displacing or degrading the extended first target-specific primer and forming a second double-stranded product comprising a barcode, wherein the second double-stranded product comprises the target polynucleotide hybridized to an extended second target-specific primer, wherein the extended second target-specific primer comprises: i) a complement of at least a portion of the target polynucleotide; and, ii) a single-stranded 5' overhang region comprising the barcode.

In some embodiments, the first target-specific primer comprises an affinity ligand and: —the extending comprises immobilizing the first double-stranded product onto a solid surface, wherein the solid surface comprises an affinity element that specifically binds the affinity ligand of the first target-specific primer; and —the removing comprises washing away non-immobilized polynucleotides. In some embodiments, the first target-specific primer is covalently attached to a solid surface and: —the hybridizing comprises contacting the solid surface to which the first target-specific primer is covalently attached to the single-stranded target polynucleotide in the reaction mixture; and —the removing comprises washing away non-immobilized polynucleotides. In some embodiments, —the extending in c) comprises extending the hybridized first target-specific primer in the presence of nucleotides that are covalently linked to an affinity ligand, thereby incorporating nucleotides linked to the affinity ligand into the extended first target-specific primer and then immobilizing the first double-stranded product onto a solid surface, wherein the solid surface comprises an affinity element that specifically binds the affinity ligand incorporated into the extended first target-specific primer; and —the removing in d) comprises washing away non-immobilized polynucleotides.

In some embodiments, the removing further comprises removing un-extended first target-specific primer, if present, by contacting the un-extended primer with a 5' to 3' single-stranded exonuclease. In some embodiments, the first target-specific primer comprises an affinity ligand and: the hybridizing a second target-specific primer comprises hybridizing the second target-specific primer to an immobilized first double-stranded product; and the extending the hybridized second target-specific primer comprises extending the second target-specific primer with the DNA polymerase comprising strand displacement activity and/or 5'-3' double-stranded exonuclease activity, thereby releasing the target polynucleotide into solution.

In some embodiments, the method further comprises: attaching (e.g., ligating or attaching by primer extension) a first and a second universal adapter to:) a first and a second end, respectively, of the second double-stranded product; or a 5' and 3' end, respectively, of a single-stranded extended second target-specific primer recovered from the second double-stranded product, or a first and a second end of a double-stranded amplification product of the recovered single-stranded extended second target-specific primer. The method can further comprise hybridizing a first universal primer to the first universal adapter and a second universal primer to the second universal adapter and extending the hybridized universal primers with a polymerase, thereby amplifying: the target polynucleotide of the universal adapter ligated second double-stranded product; or the target polynucleotide of the universal adapter ligated recovered second target-specific primer, or a double-stranded product thereof.

In some embodiments, the first or second universal adapter comprises a second barcode and the ligating the universal adapter comprising the second barcode ligates the second barcode to the extended second target-specific primer. In some embodiments, the second universal adapter is ligated to a 3' end of the recovered single-stranded extended second target-specific primer by a method comprising: i) contacting the recovered single-stranded extended second target-specific primer with a terminal transferase, thereby appending a 3' tail region comprising at least about 3, or about 8, consecutive nucleotides of the same sequence to the 3' end of the recovered single-stranded extended second target-specific primer and generating a tailed single-stranded extended second target-specific primer; ii) contacting the tailed single-stranded extended second target-specific primer with a second universal adapter comprising a double-stranded polynucleotide comprising a single-stranded 3' overhang region that is complementary to the 3' tail region of the tailed single-stranded extended second target-specific primer, thereby hybridizing the second universal adapter to the tailed single-stranded extended second target-specific primer; and iii) ligating a 5' end of the hybridized second universal adapter to the 3' tail region of the tailed single-stranded extended target-specific primer.

In some embodiments, the first universal adapter is ligated to a 5' end of the recovered single-stranded second target-specific primer by a method comprising: i) contacting the tailed or recovered single-stranded second target-specific primer with a second universal adapter comprising a double-stranded polynucleotide comprising a single-stranded 5' overhang region that is complementary to at least a portion of the barcode region of the tailed or recovered single-stranded second target-specific primer, thereby hybridizing the second universal adapter to the tailed or recovered single-stranded second target-specific primer; and iii) ligating a 3' end of the hybridized second universal adapter to a 5' end of the barcode region of the tailed or recovered single-stranded second target-specific primer. In some embodiments, the method further comprises: contacting the second double-stranded product with a universal adaptor loaded transposase to catalyze fragmentation and in vitro integration of first or second universal adapters at fragment ends; and hybridizing a first universal primer to the first universal adapters and a second universal primer to the second universal adapters and extending the hybridized universal primers with a polymerase, thereby amplifying fragments comprising first and second universal adapters.

In some embodiments: —the single-stranded target polynucleotide comprises RNA, preferably mRNA; and —the extending comprises extending the first target-specific primer with an RNA-dependent DNA polymerase to form a first double stranded product, wherein the first double-stranded product comprises a cDNA:RNA hybrid. In some embodiments, the hybridized target polynucleotide of the second double-stranded product formed by the extending of the second target-specific primer comprises a 3' single-stranded overhang region comprising at least 1 nucleotide (e.g., from 1 to 5, from 1-10, from 1-100, or from 1 to 1,000), and the method further comprises: trimming the 3' overhang region of the hybridized target polynucleotide with an enzyme comprising 3' to 5' single-stranded DNA exonuclease activity; and extending the trimmed 3' end of the hybridized target polynucleotide with a DNA polymerase, thereby incorporating a complement of the single-stranded 5' overhang region of the extended second target-specific primer that comprises the barcode into the target polynucleotide of the second double-stranded product.

In some embodiments, the method comprises: ligating a first universal adapter comprising a first universal primer binding site to the second double-stranded product formed by the extending of the second target-specific primer, the trimmed second double-stranded product formed by the ligating of the first and second universal adapters, or the trimmed and extended second double-stranded product formed by the hybridizing of the first universal primer to the first universal adaptor, wherein the first universal adapter is ligated to a 3' end of the extended second target-specific primer and the 5' end of the target polynucleotide; and ligating a second universal adapter comprising a second universal primer binding site to the single-stranded 5' overhang region of the extended second target-specific primer of the second double-stranded product formed by the extending of the second target-specific primer, the trimmed second double-stranded product formed by the ligating of the first and second universal adapters, or the trimmed and extended second double-stranded product formed the hybridizing of the first universal primer to the first universal adaptor.

In some embodiments, —the ligating of the second universal adaptor comprises ligating the second universal adapter to the second double-stranded product formed by the extending of the second target-specific primer, or the trimmed second double-stranded product formed by the ligating of the first and second universal adapters; and —the hybridizing of the first universal primer to the first universal adaptor comprises incorporating a complement of the barcode and a complement of the second universal primer binding site into the target polynucleotide of the second double-stranded product. In some embodiments, the second universal adapter is a double-stranded polynucleotide comprising a single-stranded 5' overhang region, wherein the single-stranded 5' overhang region is complementary to at least a portion of the single-stranded 5' overhang region of the extended second target-specific primer. In some embodiments, the ligating of the second universal adaptor comprises ligating a first universal adapter that is resistant to a 5' to 3' double-stranded DNA exonuclease activity, and the method further comprises: recovering the target polynucleotide comprising the complement of the barcode and the complement of the second universal primer binding site from the second double-stranded product formed by the hybridizing of the first universal primer to the first universal adaptor by contacting the second double-stranded product formed by the hybridizing of the first universal primer to the first universal adaptor with an enzyme comprising the 5' to 3' double-stranded DNA exonuclease activity, thereby degrading the extended second target-specific primer.

In some embodiments, the ligating of the second universal adapters comprises ligating a first universal adapter comprising an affinity ligand, wherein the affinity ligand is attached to a strand of the first universal adapter that is ligated to the target polynucleotide of the double-stranded product, and the method further comprises: recovering the target polynucleotide comprising the complement of the barcode and the complement of the second universal primer binding site from the second double-stranded product formed by the hybridizing of the first universal primer to the first universal adaptor by i) immobilizing the second double-stranded product to a solid surface comprising an affinity element that specifically binds the affinity ligand; and ii) eluting the extended second target-specific primer from the second double-stranded product to release the extended second target-specific primer into solution.

In some embodiments, the eluting comprises heating the second double-stranded product to a temperature sufficient

to release the extended second target specific primer into solution. In some embodiments, the temperature sufficient to release the extended second target specific primer into solution comprises a temperature of at least 75° C., 80° C., 90° C., or 95° C. In some embodiments, the eluting comprises contacting the second double-stranded product with a denaturing agent under conditions that release the extended second target specific primer into solution. In some embodiments the denaturing agent comprises an aqueous solution of an alkali hydroxide.

In some embodiments, the ligating of the second universal adaptors comprises ligating a second universal adapter comprising an affinity ligand, wherein the affinity ligand is attached to a strand of the second universal adapter that is ligated to the extended second target-specific primer, and the method further comprises: recovering the target polynucleotide comprising the complement of the barcode and the complement of the second universal primer binding site from the second double-stranded product formed by the hybridizing of the first universal primer to the first universal adaptor by i) immobilizing the second double-stranded product to a solid surface comprising an affinity element that specifically binds the affinity ligand; and ii) eluting the target polynucleotide from the second double-stranded product to release the target polynucleotide into solution. In some embodiments, the eluting comprises heating the second double-stranded product to a temperature sufficient to release the target polynucleotide into solution. In some embodiments, the temperature sufficient to release the target polynucleotide into solution comprises a temperature of at least 75° C., 80° C., 90° C., or 95° C.

In some embodiments, the eluting comprises contacting the second double-stranded product with a denaturing agent under conditions that release the target polynucleotide into solution. In some embodiments, the denaturing agent comprises an aqueous solution of an alkali hydroxide. In some embodiments, the ligating of the second universal adaptors comprises ligating a first or second universal adapter comprising a label to the second double-stranded product formed by the hybridizing of the first universal primer to the first universal adaptor, and the method further comprises: recovering the second double-stranded product formed by the hybridizing of the first universal primer to the first universal adaptor by i) immobilizing the universal adapter comprising the label, thereby immobilizing the second double-stranded product; ii) washing the immobilized second double-stranded product; and iii) eluting the second double-stranded product into solution.

In some embodiments, the label of the labeled first or second universal adapter comprises an affinity ligand, the immobilizing comprises contacting the affinity ligand to a solid surface comprising an affinity element that specifically binds the affinity ligand, and the eluting comprises contacting the immobilized second-double stranded product with a denaturing agent under conditions sufficient to disrupt the affinity ligand: affinity element interaction and release the second double-stranded product into solution. In some embodiments, the conditions sufficient to disrupt the affinity ligand: affinity element interaction comprise 8 M urea, 6 M guanidine, a pH of less than 2.0, or a pH of greater than 10.0 (e.g., a pH of or about 11, or 12).

In some embodiments, the label of the labeled first or second universal adapter is covalently attached via a linker to a solid surface before or after ligation to the second double-stranded product, and the eluting comprises cleaving the linker to release the second double-stranded product into solution. In some embodiments, the cleavage agent is a thiol

that cleaves a disulfide linker to release the second double-stranded product into solution. In some embodiments, the second universal adapter comprises a second barcode, ligating the second universal adapter comprising the second barcode ligates the second barcode to the extended second target-specific primer, and extending the trimmed 3' end of the hybridized target polynucleotide with the DNA polymerase incorporates a complement of the second barcode into the target polynucleotide. In some embodiments, the method further comprises hybridizing a first and second universal primer to the first and second universal adapters respectively, and extending the universal primers with a polymerase, thereby amplifying the target polynucleotide.

In another aspect, the present invention provides a method for enriching a plurality of structurally different target polynucleotides from a sample, wherein the method comprises performing any one of the foregoing embodiments for each structurally different target polynucleotide, wherein the hybridizing of the first target-specific primer to the single-stranded target polynucleotide comprises hybridizing a plurality of structurally different first target-specific primers to the plurality of structurally different single-stranded target polynucleotides in a single reaction mixture. In some embodiments, the method comprises attaching a first and a second universal adapter to at least a portion of the plurality of the target polynucleotides or a plurality of second target-specific primer extension products by ligation or Tn5 transposase-mediated attachment.

In yet another aspect, the present invention provides a method for sequencing a plurality of target polynucleotides from a sample comprising the plurality of target polynucleotides and a plurality of non-target polynucleotides, the method comprising: enriching the target polynucleotides from the sample by performing one or more of the foregoing methods to produce an enriched and adapter-attached sample; and sequencing the enriched and adapter-attached sample. In some embodiments, the percent of on-target reads from the enriched and adapter ligated sample is at least about 10%, at least about 15%, at least about 25%, at least about 50%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95%. In some embodiments, the percent of on-target reads from the enriched and adapter ligated sample is from about 25% to about 99%, from about 50% to about 99%, from about 50% to about 90%, from about 50% to about 85%, from about 65% to about 99%, from about 65% to about 90%, from about 65% to about 85%, from about 75% to about 99%, from about 75% to about 90%, or from about 75% to about 85%.

In some embodiments, the method comprises a step of removing the extended second target-specific primer from the second double-stranded product using an endonuclease. In some embodiments, extending the hybridized second target-specific primer is performed in the presence of one or more non-conventional nucleotides. In some embodiments, the non-conventional base introduces an abasic site that can be specifically cleaved without cleaving DNA in the same reaction. Exemplary enzymes that cleave abasic sites include, e.g., Tth Endonuclease IV, Endonuclease IV or Endonuclease VIII. In some embodiments, the non-conventional base that introduces the basic site is Int 1',2'-Dideoxyribose. Other non-conventional bases can be selected from, e.g., deoxyuracil and deoxyinosine. In some embodiments, the extended second target-specific primer contains deoxyinosine and is removed from the second double-stranded product using endonuclease V; and in other embodiments, the extended second target-specific primer

contains deoxyuracil and is removed from the second double-stranded product using uracil-N-DNA glycosylase and endonuclease VIII.

In some embodiments, the universal adaptor comprises one or more non-conventional nucleotides selected from deoxyuracil, deoxyinosine, and Int 1',2'-Dideoxyribose, and prior to universal amplification, the sample is contacted with an endonuclease. In some embodiments, the universal adaptor contains deoxyinosine and is removed from the second double-stranded product using endonuclease V; and in other embodiments, the universal adaptor contains deoxyuracil and is removed from the second double-stranded product using uracil-N-DNA glycosylase and endonuclease VIII.

In some embodiments, the first target-specific primer is part of an oligonucleotide having a 3' end and a 5' end, the first target-specific primer is at the 3' end of the oligonucleotide, and the oligonucleotide further comprises the second target-specific primer, the first target-specific and the second target-specific primer are linked in the oligonucleotide by one or more non-conventional nucleotide(s), and the hybridizing of the first target-specific primer comprises hybridizing the oligonucleotide to the single-stranded target polynucleotide and before the hybridizing of the second target-specific primer, the method further comprises treating the oligonucleotide to cleave and release the second target-specific primer from the oligonucleotide, wherein the released second target-specific primer has a 3' end available for extension. In some embodiments, the non-conventional nucleotide is deoxyinosine and the endonuclease is endonuclease V. In some embodiments, the non-conventional nucleotide is deoxyuracil and the endonuclease is endonuclease VIII and the sample is further contacted with uracil-N-DNA glycosylase (UNG). In some embodiments, the non-conventional nucleotide is Int 1',2'-Dideoxyribose and the endonuclease is Tth Endonuclease IV, Endonuclease IV or Endonuclease VIII.

In some embodiments, the method comprises attaching universal adaptors to: target polynucleotides (e.g., the single-stranded target polynucleotide or double-stranded polynucleotides that are later denatured or otherwise rendered single-stranded) before the hybridizing of the first target-specific primer to the single stranded target; or the hybridized target polynucleotide after the extending of the hybridized first target-specific primer and before the hybridizing of the second target-specific primer. In some embodiments, the attaching comprises ligation. In some embodiments, the attaching comprises tagmentation. In some embodiments, the universal adaptor comprises one or more barcode sequences.

Definitions

Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by a person of ordinary skill in the art. See, e.g., Lackie, *DICTIONARY OF CELL AND MOLECULAR BIOLOGY*, Elsevier (4th ed. 2007); Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, Cold Spring Harbor Lab Press (Cold Spring Harbor, N.Y. 1989). The term "a" or "an" is intended to mean "one or more." The term "comprise," and variations thereof such as "comprises" and "comprising," when preceding the recitation of a step or an element, are intended to mean that the addition of further steps or elements is optional and not excluded. Any methods, devices and materials similar or equivalent to those described herein can be used in the practice of this invention. The following definitions are

provided to facilitate understanding of certain terms used frequently herein and are not meant to limit the scope of the present disclosure.

As used herein, the term "substantially all" in reference to removing substantially all of a component of a reaction mixture means removing at least 90%, 95%, 99%, of the component from the reaction mixture.

As used herein, the term "barcode" refers to a nucleic acid sequence that can be detected and identified. Barcodes can be 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50 or more nucleotides long. Barcodes can employ error correcting codes such that one or more errors in synthesis, replication, and/or sequencing can be corrected to identify the barcode sequence. Examples of error correcting codes and their use in barcodes and barcode identification and/or sequencing include, but are not limited to, those described in U.S. 2010/0,323,348; and U.S. Pat. No. 8,715,967. In some cases, the barcodes are designed to have a minimum number of distinct nucleotides with respect to all other barcodes of a population. The minimum number can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more. Thus, for example, a population of barcodes having a minimum number of at least 5 distinct nucleotides will differ at at least 5 nucleotide positions from all other barcodes in the population.

As used herein, the term "multiplex identifier," "MID," and the like, refers to a barcode that identifies a source or sample. As such, all or substantially all, MID barcoded polynucleotides from a single source or sample will share an MID of the same sequence; while all, or substantially all (e.g., at least 90% or 99%), MID barcoded polynucleotides from different sources or samples will have a different MID barcode sequence. Polynucleotides from different sources or samples and having different MIDs can then be mixed and sequenced in parallel while maintaining source/sample information. Thus sequence reads can be assigned to individual samples.

As used herein, the term "universal identifier," "universal molecular identifier," "unique molecular identifier," "UID," and the like, refers to a barcode that identifies a polynucleotide to which it is attached. Typically, all, or substantially all (e.g., at least 90% or 99%), UID barcodes in a mixture of UID barcoded polynucleotides are unique.

The term "nucleic acid" or "polynucleotide" refers to deoxyribonucleic acids (DNA) or ribonucleic acids (RNA) and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions), alleles, orthologues, SNPs, and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., *Nucleic Acid Res.* 19:5081 (1991); Ohtsuka et al., *J. Biol. Chem.* 260:2605-2608 (1985); and Rossolini et al., *Mol. Cell. Probes* 8:91-98 (1994)).

"Polymerase" refers to an enzyme that performs template-directed synthesis of polynucleotides. A DNA polymerase can add free nucleotides only to the 3' end of the newly forming strand. This results in elongation of the newly

forming strand in a 5'-3' direction. No known DNA polymerase is able to begin a new chain (de novo). DNA polymerase can add a nucleotide only on to a pre-existing 3'-OH group, and, therefore, needs a primer at which it can add the first nucleotide. Non-limiting examples of poly-

merases include prokaryotic DNA polymerases (e.g. Pol I, Pol II, Pol III, Pol IV and Pol V), eukaryotic DNA polymerase, archaeal DNA polymerase, telomerase, reverse transcriptase and RNA polymerase. Reverse transcriptase is an RNA-dependent DNA polymerase which synthesizes DNA from an RNA template. The reverse transcriptase family contain both DNA polymerase functionality and RNase H functionality, which degrades RNA base-paired to DNA. RNA polymerase, is an enzyme that synthesizes RNA using DNA as a template during the process of gene transcription. RNA polymerase polymerizes ribonucleotides at the 3' end of an RNA transcript.

In some embodiments, a polymerase from the following may be used in a polymerase-mediated primer extension, end-modification (e.g., terminal transferase, degradation, or polishing), or amplification reaction: archaea (e.g., *Thermococcus litoralis* (Vent, GenBank: AAA72101), *Pyrococcus furiosus* (Pfu, GenBank: D12983, BAA02362), *Pyrococcus woessii*, *Pyrococcus* GB-D (Deep Vent, GenBank: AAA67131), *Thermococcus kodakaraensis* KOD1 (KOD, GenBank: BD175553, BAA06142; *Thermococcus* sp. strain KOD (Pfx, GenBank: AAE68738)), *Thermococcus gorgonarius* (Tgo, Pdb: 4699806), *Sulfolobus solataricus* (GenBank: NC002754, P26811), *Aeropyrum pernix* (GenBank: BAA81109), *Archaeoglobus fulgidus* (GenBank: 029753), *Pyrobaculum aerophilum* (GenBank: AAL63952), *Pyrodictium occultum* (GenBank: BAA07579, BAA07580), *Thermococcus* 9 degree Nm (GenBank: AAA88769, Q56366), *Thermococcus fumicolans* (GenBank: CAA93738, P74918), *Thermococcus hydrothermalis* (GenBank: CAC18555), *Thermococcus* sp. GE8 (GenBank: CAC12850), *Thermococcus* sp. JDF-3 (GenBank: AX135456; WO0132887), *Thermococcus* sp. TY (GenBank: CAA73475), *Pyrococcus abyssi* (GenBank: P77916), *Pyrococcus glycovorans* (GenBank: CAC12849), *Pyrococcus horikoshii* (GenBank: NP 143776), *Pyrococcus* sp. GE23 (GenBank: CAA90887), *Pyrococcus* sp. ST700 (GenBank: CAC 12847), *Thermococcus pacificus* (GenBank: AX411312.1), *Thermococcus zilligii* (GenBank: DQ3366890), *Thermococcus aggregans*, *Thermococcus barossii*, *Thermococcus celer* (GenBank: DD259850.1), *Thermococcus profundus* (GenBank: E14137), *Thermococcus siculi* (GenBank: DD259857.1), *Thermococcus thioreducens*, *Thermococcus onnurineus* NA1, *Sulfolobus acidocaldarium*, *Sulfolobus tokodaii*, *Pyrobaculum calidifontis*, *Pyrobaculum islandicum* (GenBank: AAF27815), *Methanococcus jannaschii* (GenBank: Q58295), *Desulforococcus* species TOK, *Desulforococcus*, *Pyrolobus*, *Pyrodictium*, *Staphylothermus*, *Vulcanisaetta*, *Methanococcus* (GenBank: P52025) and other archaeal B polymerases, such as GenBank AAC62712, P956901, BAAA07579), thermophilic bacteria *Thermus* species (e.g., *flavus*, *ruber*, *thermophilus*, *lacteus*, *rubens*, *aquaticus*), *Bacillus stearothermophilus*, *Thermotoga maritima*, *Methanothermobacter fervidus*, KOD polymerase, TNA1 polymerase, *Thermococcus* sp. 9 degrees N-7, T4, T7, phi29, *Pyrococcus furiosus*, *P. abyssi*, *T. gorgonarius*, *T. litoralis*, *T. zilligii*, *T. sp. GT*, *P. sp. GB-D*, KOD, Pfu, *T. gorgonarius*, *T. zilligii*, *T. litoralis* and *Thermococcus* sp. 9N-7 polymerases.

The term "thermostable polymerase," refers to an enzyme that is stable to heat, is heat resistant, and retains sufficient activity to effect subsequent polynucleotide extension reactions and does not become irreversibly denatured (inacti-

vated) when subjected to the elevated temperatures for the time necessary to effect denaturation of double-stranded nucleic acids. The heating conditions necessary for nucleic acid denaturation are well known in the art and are exemplified in, e.g., U.S. Pat. Nos. 4,683,202, 4,683,195, and 4,965,188, which are incorporated herein by reference. As used herein, a thermostable polymerase is suitable for use in a temperature cycling reaction such as the polymerase chain reaction ("PCR"), a primer extension reaction, or an end-modification (e.g., terminal transferase, degradation, or polishing) reaction. Irreversible denaturation for purposes herein refers to permanent and complete loss of enzymatic activity. For a thermostable polymerase, enzymatic activity refers to the catalysis of the combination of the nucleotides in the proper manner to form polynucleotide extension products that are complementary to a template nucleic acid strand. Thermostable DNA polymerases from thermophilic bacteria include, e.g., DNA polymerases from *Thermotoga maritima*, *Thermus aquaticus*, *Thermus thermophilus*, *Thermus flavus*, *Thermus filiformis*, *Thermus* species sps17, *Thermus* species Z05, *Thermus caldophilus*, *Bacillus caldotenax*, *Thermotoga neopolitana*, *Thermosiphon africanus*, and other thermostable DNA polymerases disclosed above.

In some cases, the nucleic acid (e.g., DNA or RNA) polymerase may be a modified naturally occurring Type A polymerase. A further embodiment of the invention generally relates to a method wherein a modified Type A polymerase, e.g., in a primer extension, end-modification (e.g., terminal transferase, degradation, or polishing), or amplification reaction, may be selected from any species of the genus *Meiothermus*, *Thermotoga*, or *Thermomicrobium*. Another embodiment of the invention generally pertains to a method wherein the polymerase, e.g., in a primer extension, end-modification (e.g., terminal transferase, degradation, or polishing), or amplification reaction, may be isolated from any of *Thermus aquaticus* (Taq), *Thermus thermophilus*, *Thermus caldophilus*, or *Thermus filiformis*. A further embodiment of the invention generally encompasses a method wherein the modified Type A polymerase, e.g., in a primer extension, end-modification (e.g., terminal transferase, degradation, or polishing), or amplification reaction, may be isolated from *Bacillus stearothermophilus*, *Sphaerobacter thermophilus*, *Dictoglomus thermophilum*, or *Escherichia coli*. In another embodiment, the invention generally relates to a method wherein the modified Type A polymerase, e.g., in a primer extension, end-modification (e.g., terminal transferase, degradation, or polishing), or amplification reaction, may be a mutant Taq-E507K polymerase. Another embodiment of the invention generally pertains to a method wherein a thermostable polymerase may be used to effect amplification of the target nucleic acid.

As used herein the term "primer" refers to an oligonucleotide which binds to a specific region of a single-stranded template nucleic acid molecule and initiates nucleic acid synthesis via a polymerase-mediated enzymatic reaction, extending from the 3' end of the primer and complementary to the sequence of the template molecule. PCR amplification primers can be referred to as 'forward' and 'reverse' primers, one of which is complementary to a nucleic acid strand and the other of which is complementary to the complement of that strand. Typically a primer comprises fewer than about 100 nucleotides and preferably comprises fewer than about 30 nucleotides. Exemplary primers range from about 5 to about 25 nucleotides. Primers can comprise, for example, RNA and/or DNA bases, as well as non-naturally-occurring bases. The directionality of the newly forming strand (the daughter strand) is opposite to the direction in which DNA

polymerase moves along the template strand. In some cases, a target-specific primer specifically hybridizes to a target polynucleotide under hybridization conditions. Such hybridization conditions can include, but are not limited to, hybridization in isothermal amplification buffer (20 mM Tris-HCl, 10 mM (NH₄)₂SO₄), 50 mM KCl, 2 mM MgSO₄, 0.1% TWEEN® 20, pH 8.8 at 25° C.) at a temperature of about 40° C., 45° C., 50° C., 55° C., 60° C., 65° C., or 70° C.

As used herein, the term “universal primer” and “universal primers” refers to a primer that can hybridize to and support amplification of target polynucleotides having a shared complementary universal primer binding site. Similar, the term “universal primer pair” refers to a forward and reverse primer pair that can hybridize to and support PCR amplification of target polynucleotides having shared complementary forward and reverse universal primer binding sites. Such universal primer(s) and universal primer binding site(s) can allow single or double-primer mediated universal amplification (e.g., universal PCR) of target polynucleotide regions of interest.

As used herein the term “sample” refers to any biological sample that comprises nucleic acid molecules, typically comprising DNA and/or RNA. Samples may be tissues, cells or extracts thereof, or may be purified samples of nucleic acid molecules. Use of the term “sample” does not necessarily imply the presence of target sequence within nucleic acid molecules present in the sample.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A-E illustrate an embodiment of unidirectional double primer extension target enrichment (UD-PETE). In the embodiment illustrated, the first primer extension product is hybridized to a target polynucleotide and extended with a polymerase (FIG. 1A). The first primer, and thus the first primer extension product, is biotinylated. Biotinylated first primer, or first primer extension product is captured onto an anti-biotin (e.g., streptavidin) coated solid surface and hybridization (FIG. 1B) and extension of the second target-specific primer releases target polynucleotide away from the immobilized first primer extension product (FIG. 1C). A first and second adapter containing a first and second universal primer binding site respectively can be ligated to the second target-specific primer extension product (FIG. 1D). The adapter ligated extension product can be amplified by universal PCR (FIG. 1E).

FIGS. 2A-E illustrate an alternate embodiment of UD-PETE. In this embodiment, a double-stranded polynucleotide containing the single-stranded target polynucleotide hybridized to the second target-specific primer extension product is ligated to an adapter containing a universal primer hybridization site (FIG. 2D) and digested at an unhybridized 3' single-stranded overhang region of the target polynucleotide with an enzyme that exhibits 3' to 5' single-stranded exonuclease activity (FIG. 2E).

FIGS. 3A-D illustrate methods of incorporating MID and UID barcodes into the original target polynucleotide and recovering the barcoded original single-stranded target polynucleotide and removing the hybridized second target-specific primer extension product.

FIG. 4 illustrates the results of incorporating cleavable nucleotides according to the method of the invention.

FIG. 5 illustrates an alternate embodiment of UD-PETE. In this embodiment, an oligonucleotide comprising a first target-specific primer sequence is linked to a second target-specific primer sequence by one or more non-conventional bases (also referred to herein as “modified bases.”) The

oligonucleotide is hybridized to a target polynucleotide and extended with a polymerase to form the first primer extension product (top panel). The oligonucleotide, and thus the first primer extension product, is optionally biotinylated. Biotinylated oligonucleotide or first primer extension product is optionally captured onto an anti-biotin (e.g., streptavidin) coated solid surface. The first primer extension primer is contacted with an endonuclease that targets the non-conventional base(s) to release the second target-specific primer sequence having a 3'—OH. The second target-specific primer can then be hybridized to the target polynucleotide and extended with a polymerase having strand displacement activity to generate a second primer extension product. The first primer extension product is thus displaced or digested. Universal adapters can be subsequently added to the second primer extension product, (not depicted in FIG. 5) as shown for example in FIGS. 1D-E.

FIG. 6 illustrates an alternate embodiment of that shown in FIG. 0.5, wherein a non-target polynucleotide is hybridized with the oligonucleotide. The first primer sequence hybridizes to the non-target polynucleotide but that second primer sequence does not hybridize and thus a second primer extension product is not formed.

FIGS. 7A-B depict On-Target Rate and Coverage Uniformity as described in Example 2.

FIGS. 8A-B depict sequencing results from Example 3: on target rate and genome equivalent recovery (GER) (FIG. 8A), and probe coverage uniformity (FIG. 8B).

FIG. 9 depicts Cts of an amplification reaction from Example 3.

FIGS. 10A-B depict sequencing results from Example 4: on target rate and genome equivalent recovery (GER) (FIG. 10A), and probe coverage uniformity (FIG. 10B).

FIGS. 11A-B depict sequencing results from Example 5: on target rate and genome equivalent recovery (GER) (FIG. 11A), and probe coverage uniformity (FIG. 11B).

DETAILED DESCRIPTION OF THE INVENTION

I. Introduction

The present invention provides a primer extension target enrichment (PETE) method that includes two unidirectional primers and compositions for performing and using the unidirectional double primer PETE (UD-PETE) method. The use of two unidirectional primers increases the stringency of the enrichment step as compared to methods that require only a single primer or single bait for enrichment of each structurally distinct target polynucleotide. Thus, in some cases, the UD-PETE method provides improved or synergistic target enrichment in comparison to other target enrichment methods such as, e.g., single primer extension target enrichment methods.

Moreover, in contrast to multiplex PCR based methods in which multiple first and second amplification primers are in the same reaction mixture at the same time, the UD-PETE method can include a step of removing un-extended first primers before introducing second primers into a reaction mixture. Thus, in some cases, the method can reduce or eliminate competition between first and second primers. As such, in some cases, the first or second primers, or both can be used at significantly higher concentrations in the UD-PETE reaction mixture as compared to, e.g., multiplex PCR based methods. Additionally, or alternatively, an increased

number of first or second primers can be used in the FP-PETE reaction mixture as compared to, e.g., multiplex PCR based methods.

In one embodiment, a first primer is hybridized to a 3' region of a single-stranded target polynucleotide and extended with a DNA polymerase. A second primer can be hybridized to a 3' region of the same single-stranded target polynucleotide that is 3' of the region to which the first primer hybridized. The second primer can then be extended with a DNA polymerase. Thus, the first and second primer are both hybridized to the same end and extended in the same direction (i.e., unidirectionally) relative to the target polynucleotide.

In a further embodiment, the first target-specific primer sequence and the second target-specific primer sequence can be provided as parts of a single oligonucleotide wherein the first target-specific primer sequence and the second target-specific primer sequence are linked and separated by at least one non-conventional base (e.g., selected from deoxyuracil, deoxyinosine, Int 1',2'-Dideoxyribose) that can be cleaved without cleaving naturally-occurring DNA in the same reaction. The oligonucleotide is used as the first-target-specific primer in a first extension reaction. After the first extension reaction is completed, the oligonucleotide can be treated with an endonuclease that targets the non-conventional base(s) to release the second target-specific primer sequence, which will have a 3'-OH end that is available for primer extension. The second target-specific primer can then be used in a strand displacement reaction as described above and elsewhere herein to generate the second target-specific primer extension product.

II. Methods

Described herein are unidirectional double primer extension target enrichment methods (UD-PETE) for enriching a target polynucleotide from a sample.

a. Forming a First Primer Extension Product

In some embodiments, the methods include a) providing a reaction mixture containing the sample and a first target-specific primer, wherein the sample contains a single-stranded target polynucleotide having 3' and a 5' end and a plurality of structurally different single-stranded non-target polynucleotides. In some embodiments, the methods further include b) hybridizing a first target-specific primer to the single-stranded target polynucleotide in the reaction mixture. Generally, the first target-specific primer is hybridized to a first hybridizing region of the single-stranded target polynucleotide that is far enough in the 5' direction from the 3' end of the single-stranded target polynucleotide that a second unidirectional primer can be hybridized to second hybridizing region of the target polynucleotide that is 3' of the first hybridizing region and does not overlap with the first hybridizing region. For example in some cases, the first target-specific primer hybridizes at least 6 nucleotides from the 3' end of the single-stranded target polynucleotide. In some cases, the first target-specific primer hybridizes at least 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides from the 3' end of the single-stranded target polynucleotide. The target polynucleotide can in some embodiments comprise universal adaptor sequences on either end of the polynucleotide.

In some cases, the first target-specific primer hybridizes to the 5'-most nucleotide of the target polynucleotide. In some cases, the first target-specific primer hybridizes to the penultimate 5' nucleotide of the target polynucleotide, but not the 5'-most nucleotide of the target polynucleotide. In some

cases, the first target-specific primer hybridizes to a region that is within 10 or 100 nucleotides of the 5'-most nucleotide of the target polynucleotide. In some cases, the first target-specific primer hybridizes to a region that is at least 6 nucleotides from the 3' end of the target polynucleotide and more than 100 nucleotides 3' to the 5'-most nucleotide of the target polynucleotide.

In some cases, the first target-specific primer hybridizes to a region of the target polynucleotide that is at least 6 nucleotides and no more than 500 nucleotides from the 3' end of the target polynucleotide, at least 8 nucleotides and no more than 500 nucleotides from the 3' end of the target polynucleotide, at least 10 nucleotides and no more than 500 nucleotides from the 3' end of the target polynucleotide, at least 12 nucleotides and no more than 500 nucleotides from the 3' end of the target polynucleotide, at least 15 nucleotides and no more than 500 nucleotides from the 3' end of the target polynucleotide, or at least 20 nucleotides and no more than 500 nucleotides from the 3' end of the target polynucleotide. In some cases, the first target-specific primer hybridizes to a region of the target polynucleotide that is at least 6 nucleotides and no more than 100 nucleotides from the 3' end of the target polynucleotide, at least 8 nucleotides and no more than 100 nucleotides from the 3' end of the target polynucleotide, at least 10 nucleotides and no more than 100 nucleotides from the 3' end of the target polynucleotide, at least 12 nucleotides and no more than 100 nucleotides from the 3' end of the target polynucleotide, at least 15 nucleotides and no more than 100 nucleotides from the 3' end of the target polynucleotide, at least 20 nucleotides and no more than 100 nucleotides from the 3' end of the target polynucleotide, at least 6 nucleotides and no more than 50 nucleotides from the 3' end of the target polynucleotide, at least 8 nucleotides and no more than 50 nucleotides from the 3' end of the target polynucleotide, at least 10 nucleotides and no more than 50 nucleotides from the 3' end of the target polynucleotide, at least 12 nucleotides and no more than 50 nucleotides from the 3' end of the target polynucleotide, at least 15 nucleotides and no more than 50 nucleotides from the 3' end of the target polynucleotide, or at least 20 nucleotides and no more than 50 nucleotides from the 3' end of the target polynucleotide.

In some embodiments, the method further includes c) extending the hybridized first target-specific primer with a DNA polymerase to form a first double-stranded product comprising the target polynucleotide hybridized to the extended first target-specific primer. The hybridized target polynucleotide of the double-stranded product can include a single-stranded overhang region at the 3' end. The length of the single-stranded overhang region at the 3' end can be, at least in part, determined by the distance between the 3' end and the position at which the first target-specific primer hybridizes to the target polynucleotide. Thus, a first target-specific primer that hybridizes at least 6 nucleotides from the 3' end of the single-stranded target polynucleotide and is subsequently extended by a DNA polymerase can produce a double-stranded product having a hybridized target polynucleotide with a single-stranded overhang region of at least 6 consecutive nucleotides at the 3' end.

As such, in some cases, the single-stranded overhang region of the double-stranded product produced by extension of the first target-specific primer can have a length of, or of at least, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides. In some cases, the single-stranded overhang region of the double-stranded product produced by extension of the first target-specific primer can have a length of, or of at least, 6

to 500, 8 to 500, 10 to 500, 12 to 500, 15 to 500, 20 to 500, 6 to 100, 8 to 100, 10 to 100, 12 to 100, 15 to 100, 20 to 100, 6 to 50, 8 to 50, 10 to 50, 12 to 50, 15 to 50, or 20 to 50 nucleotides. In some cases, the single-stranded overhang region of the double-stranded product produced by extension of the first target-specific primer can have a length of at least 40; 50; 100; 250; 500; 1,000; or 10,000 nucleotides.

In some embodiments, the method includes d) removing single-stranded target and non-target polynucleotides that are not hybridized to extended target-specific primer, if present from the reaction mixture. In some cases, the removing of d) includes removing un-extended first target-specific primers. In some cases, the removing of d) includes contacting single-stranded target and non-target polynucleotides with a 5' to 3' single-stranded exonuclease. In some cases, the removing of d) includes contacting single-stranded target and non-target polynucleotides, including un-extended first target-specific primers with a 5' to 3' single-stranded exonuclease.

In some embodiments, the first target-specific primers are labeled first target-specific primers, wherein the label is an affinity ligand covalently linked to the primer. Exemplary affinity ligands include, but are not limited to, biotin or a derivative thereof, such as iminobiotin. In some cases, the labeled first target-specific primers are immobilized to a solid surface. The labeled first target-specific primers can be immobilized before or after, or at the same time as, hybridizing to the single-stranded target polynucleotide in the reaction mixture. Alternatively, the labeled first target-specific primers can be immobilized after hybridizing to the single-stranded target polynucleotide in the reaction mixture and extending the hybridized first target-specific primer with the DNA polymerase.

In some embodiments, the first target-specific primer is covalently linked to an affinity ligand, hybridized to the target polynucleotide, and extended with a polymerase to produce an immobilized double-stranded product. In such embodiments, the removing single-stranded target and non-target polynucleotides that are not hybridized to extended target-specific primer of d) can include washing away non-immobilized polynucleotides. In some cases, the removing single-stranded target and non-target polynucleotides that are not hybridized to extended target-specific primer of d) can include removing the immobilized double-stranded product from the reaction mixture; and, optionally, placing the immobilized double-stranded product into a different reaction mixture.

In some embodiments, the first target-specific primers are not labeled with an affinity ligand and at least some free nucleotides are provided that are linked to an affinity label such that at least some nucleotides that are incorporated into the extended target-specific primer are covalently linked to an affinity label, for example an affinity ligand including, but not limited to, biotin or a derivative thereof, such as iminobiotin.

In some embodiments, universal adapter sequences can be attached to the double-stranded product prior to formation of the second primer extension product discussed below. For example, universal adapter sequences can be attached by ligation. In some embodiments, the universal adapter sequences can include one or more barcode sequences (e.g., a sample (MID) barcode).

In some embodiments, the first target-specific primer sequence (as described above) is provided as a 3' sequence of an oligonucleotide that also comprises the second target-specific primer sequence at the 5' end of the oligonucleotide. The first and second target-specific primer sequences are

linked and separated by one or more non-conventional bases that can be cleaved without cleaving the DNA in the reaction. Exemplary non-conventional bases can include but are not limited to deoxyuracil, deoxyinosine, and Int 1',2'-Dideoxyribose. The oligonucleotide can then hybridized to a target polynucleotide and extended with a polymerase to form the first primer extension product. As discussed elsewhere subsequently, the oligonucleotide can be cleaved to release the second target-specific primer from the oligonucleotide, thereby allowing the second target-specific primer to be available for primer extension.

b. Forming a Second Primer Extension Product

In some embodiments, the method further includes e) hybridizing a 3' hybridizing region of a second target-specific primer to the single-stranded overhang region at the 3' end of the hybridized target polynucleotide. In some cases, the second target-specific primer contains a 3' hybridizing region that hybridizes to the target polynucleotide and a 5' region that does not hybridize to the target polynucleotide. In some cases, the 5' region that does not hybridize to the target polynucleotide contains a barcode (e.g., a UID barcode) region. In some cases, the second target-specific primer contains a 5'-terminal phosphate. In such embodiments, a polymerase extension product of the second target-specific primer can therefore contain a 5'-terminal phosphate.

In some cases, the 5' region that does not hybridize to the target polynucleotide additionally, or alternatively, contains a [SPLINT] region. The [SPLINT] region can include an adapter hybridization site of at least 2 nucleotides in length. In some cases, the adapter hybridization site is at least 4 nucleotides in length, at least 6 nucleotides in length, at least 8 nucleotides in length, from 2 to 10 nucleotides in length, or from 2 to 8 nucleotides in length. The [SPLINT] region can be complementary to a single-stranded 5' overhang region of a double-stranded adapter, such that when the single-stranded 5' overhang region of the double-stranded adapter hybridizes to the [SPLINT] region, a 3'-OH of the adapter can be ligated to a 5' terminal phosphate of a second target-specific primer or an extended second target-specific primer (e.g., an extended second target-specific primer hybridized to a target polynucleotide). In some embodiments, [SPLINT] comprises or consists of 6 consecutive nucleotides that are complementary to a single-stranded 5' overhang region of a double-stranded adapter. In some embodiments, [SPLINT] comprises or consists of the sequence CGA TCT.

In some embodiments, the nucleotide at the 3' end of the second target-specific primer hybridizes to the 5'-most nucleotide of the single-stranded overhang region. In some cases, the nucleotide at the 3' end of the second target-specific primer hybridizes to a nucleotide of the single-stranded overhang region of the hybridized target polynucleotide that is at least 1 nucleotide 3' of the 5'-most nucleotide of the single-stranded overhang region. In some cases, the nucleotide at the 3' end of the second target-specific primer hybridizes to a nucleotide of the single-stranded overhang region of the hybridized target polynucleotide that is, or is at least, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides 3' of the 5'-most nucleotide of the single-stranded overhang region.

In some cases, the gap on the target polynucleotide between the 3' end of the second target-specific primer hybridized to the target polynucleotide and the 5'-most nucleotide of the first target-specific primer (e.g., extended first target-specific primer) that is hybridized to the target

polynucleotide is from 0 to about 10,000 or more nucleotides, from about 1 to about 10,000 or more nucleotides, from 0 to about 1,000 or more nucleotides, from 1 to about 1,000 or more nucleotides, from about 1 to about 500 nucleotides, from about 3 to about 500 nucleotides, from about 5 to about 500 nucleotides, or from about 10 to about 500 nucleotides in length. In some cases, the gap is less than 1,000; 500; 250; 100; 50; or 10 nucleotides in length.

In some cases, the second target-specific primer hybridizes to a region of the target polynucleotide that overlaps with the region to which the first target-specific primer hybridizes. The number of overlapping targeted nucleotides (nucleotides of the target polynucleotide that hybridize to both first and second target-specific primer) can be 0 (i.e., no overlap), 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12, e.g., from about 1 to about 12, from about 1 to about 10, from about 1 to about 8, from about 1 to about 6, or from about 1 to about 4.

In some embodiments, the method further comprises f) extending the hybridized second target-specific primer with a DNA polymerase, thereby forming a second double-stranded product that contains the target polynucleotide hybridized to an extended second target-specific primer. The second double-stranded product can have a 3' single-stranded overhang region, a 5' single-stranded overhang region, or a combination thereof.

For example, in some cases, the second target-specific primer hybridizes to a region of the target polynucleotide that is, or is at least, one nucleotide 5' of the 3' end of the target polynucleotide. In such cases, the second double-stranded product can contain a 3' single-stranded overhang region having a length of, or of at least, one nucleotide. In some cases, the 3' single-stranded overhang region of the second double-stranded product can have a length of, or of at least, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides. In some cases, the 3' single-stranded overhang region of the second double-stranded product can have a length of, or of at least, 6 to 500, 8 to 500, 10 to 500, 12 to 500, 15 to 500, 20 to 500, 6 to 100, 8 to 100, 10 to 100, 12 to 100, 15 to 100, 20 to 100, 6 to 50, 8 to 50, 10 to 50, 12 to 50, 15 to 50, or 20 to 50 nucleotides.

As described above, the second target-specific primer can contain a 3' hybridizing region that hybridizes to the target polynucleotide and a 5' region that does not hybridize to the target polynucleotide. In such cases, the second double-stranded product produced by extending hybridized second target-specific primer can contain a 5' single-stranded overhang region corresponding to the 5' region of the primer that does not hybridize to the target polynucleotide. In some cases, the 5' region of the primer that does not hybridize to the target polynucleotide contains a barcode (e.g., a UID barcode). In such cases, the extending of the second target-specific primer can thereby produce a second double-stranded product containing the target polynucleotide hybridized to the extended second target-specific primer, wherein the extended second target-specific primer comprises a complement of at least a portion of the target polynucleotide, and a single-stranded 5' overhang region comprising the barcode.

In some cases, the DNA polymerase exhibits strand displacement activity. In some cases, the DNA polymerase exhibits 5'-3' DNA exonuclease activity that digests a single strand of a double-stranded DNA substrate (referred to herein as 5'-3' double-stranded DNA exonuclease activity) or double-stranded DNA exonuclease activity. In some cases, the DNA polymerase exhibits both strand displace-

ment and 5'-3' double-stranded DNA exonuclease activity. In some cases, the strand displacement, 5'-3' double-stranded DNA exonuclease activity, or combination thereof, can displace target polynucleotide (e.g., original target polynucleotide molecule from a provided sample) into solution.

For example, in some cases, a first double-stranded product containing the target polynucleotide hybridized to the extended first target-specific primer is immobilized on a solid surface, e.g., by affinity capture of a ligand (e.g., biotin or a derivative thereof) covalently linked to the extended first target-specific primer. In such cases, the strand displacement activity of the DNA polymerase that extends the hybridized second target-specific primer displaces the target polynucleotide from the sample into solution. Alternatively, 5'-3' exonuclease activity can degrade extended first target-specific primer that is immobilized by affinity capture and hybridized to target polynucleotide, wherein the 5'-3' exonuclease activity thereby releases the target polynucleotide into solution.

In some cases, single-stranded extended second target-specific primer can be recovered from the second double-stranded product, producing a recovered single-stranded extended second target-specific primer. In some cases, the extended second target-specific primer can be recovered from the second double-stranded product before attachment of a first or second universal adapter. In some cases, the extended second target-specific primer can be recovered from the second double-stranded product after attachment of a first universal adapter and before attachment of a second universal adapter. In some cases, the extended second target-specific primer can be recovered from the second double-stranded product after attachment of a first universal adapter and a second universal adapter.

For example, in some cases, the second target-specific primer is blocked at a 5' end, such that the extended second target-specific primer is resistant to 5'-3' exonuclease activity. In such cases, the second double-stranded product can be contacted with a single-stranded, double-stranded, or single and double-stranded 5'-3' exonuclease to degrade the target polynucleotide in the second double-stranded product. In some cases, the single and double-stranded 5'-3' exonuclease is provided by the same enzyme. In other cases, the contacting the second double-stranded product with a single and double-stranded 5'-3' exonuclease is performed by contacting the second double-stranded product with two different enzymes. In some cases, the target polynucleotide in the second double-stranded product is degraded by contacting with 5'-3' exonuclease activity and purifying the single-stranded extended second target-specific primer (e.g., by column, bead, resin, batch, gel, or membrane-based nucleic acid purification methods including, but not limited to, solid-phase reversible immobilization methods (SPRI)).

In some embodiments, the target polynucleotide is RNA (e.g., mRNA). In such embodiments, extending the hybridized first target-specific primer is performed with an RNA-dependent DNA polymerase, and the first double-stranded product thus formed is a cDNA/RNA hybrid. Similarly, extending the hybridized second target-specific primer thus forms a second double-stranded product that is also a cDNA/RNA hybrid. In such cases, the extended second target-specific primer can be recovered by digesting the RNA of the cDNA/RNA hybrid with an enzyme that exhibits RNase H activity.

In embodiments in which the first and second target specific primers are provided as parts of a single oligonucleotide (with the first target-specific primer sequencing being at the 3' end of the oligonucleotide), the first and second

target-specific primers sequences can be separated following initial priming based on the first target-specific primer sequence. See, e.g., FIG. 5. For example, one or more non-conventional bases separating the first and second target-specific primer sequences can be cleaved to separate the second target-specific primer sequence from the first target-specific primer sequence, leaving a 3'—OH moiety on the second target-specific primer to allow for subsequent primer extension from the second target-specific primer. For example, an endonuclease that targets the non-conventional base can be used to release the second primer from the oligonucleotide such that the second primer has a free 3'—OH. Tth Endonuclease IV, Endonuclease IV or Endonuclease VIII. Exemplary endonucleases can include but are not limited to, Tth Endonuclease IV, Endonuclease IV, or *E. coli* endonuclease VIII (which cleave at abasic sites) or *E. coli* endonuclease V (which cleaves at deoxyinosine sites). In the embodiment where deoxyuracil is incorporated, the reaction mixture can be contacted with uracil-N-DNA glycosylase (UNG). UNG cleaves the uracil from DNA leaving an abasic site. In some embodiments, the non-conventional base that introduces the abasic site is Int 1',2'-Dideoxyribose. The sample can then be further contacted with an endonuclease cleaving the DNA at abasic sites. The released second target-specific primer can then be hybridized to the target polynucleotide and extended with a polymerase having strand displacement activity as described above, thereby releasing or removing the first primer extension product and generating the second primer extension product.

c. Attachment of Universal Adapters

In some embodiments, the methods further include attaching a first universal adapter, or a first and second universal adapter to the second double-stranded product. Additionally or alternatively, the methods further include attaching a first universal adapter, or a first and second universal adapter to a recovered single-stranded extended second target-specific primer. In some cases, the first universal adapter is attached to the second double-stranded product, the first adapter-attached extended second target-specific primer is recovered from the double-stranded product, and a second universal adapter is attached to the first adapter-attached and recovered single-stranded extended second target-specific primer.

In some cases, attachment of a first universal adapter, second universal adapter, or the combination thereof includes ligating the one or more adapter(s) to the second double-stranded product, or recovered single-stranded extended second target-specific primer. In some cases, the ligation can require a 5'-terminal phosphate on a donor strand. In some cases a 5'-terminal phosphate is provided by using a second target-specific primer having a 5'-terminal phosphate. In some cases, a 5'-terminal phosphate is provided by contacting the second double-stranded product, or recovered single-stranded extended second target-specific primer with an enzyme that can append a 5'-terminal phosphate to a polynucleotide (e.g., T4 polynucleotide kinase or a 3' phosphatase minus derivative thereof).

In some cases, a first universal adapter is attached to a recovered single-stranded extended second target-specific primer by ligation. For example, a first universal adapter can be a splint adapter that is ligated to a recovered single-stranded extended second target-specific primer. Splint adapters can contain a double stranded region and a 5' single-stranded overhang region, wherein the 5' single-stranded overhang region is complementary to and hybridizes under hybridization conditions with the [SPLINT] region of the recovered single-stranded extended second target-specific primer. The splint adapter can be configured

to hybridize to the [SPLINT] region such that a 3'—OH of the adapter (e.g., on the opposite strand as the 5' single-stranded overhang region of the splint adapter) can be ligated to a 5'-terminal phosphate of the recovered single-stranded extended second target-specific primer. The 5' single-stranded overhang region of the splint adapter can be at least 2 nucleotides in length, at least 4 nucleotides in length, at least 6 nucleotides in length, at least 8 nucleotides in length, from 2 to 10 nucleotides in length, or from 2 to 8 nucleotides in length. In some embodiments, the 5' single-stranded overhang region comprises or consists of 6 consecutive nucleotides that are complementary to a [SPLINT] region of the recovered single-stranded extended second target-specific primer. In some embodiments, the 5' single-stranded overhang region comprises or consists of the sequence AGA TCG.

In some cases, the first universal adapter can contain a barcode. For example, the first universal adapter can contain an MID barcode. Thus, attachment (e.g., ligation) of a first universal adapter can attach an MID barcode, a first universal primer binding site, or a combination thereof, to the recovered single-stranded extended second target-specific primer. In some cases, the attachment (e.g., ligation) of a first universal adapter can attach an MID barcode, a first universal primer binding site, or a combination thereof, to the second double-stranded product.

In some cases, a second universal adapter is attached to a recovered single-stranded extended second target-specific primer (e.g., after attachment of first universal adapter) by ligation. For example, a 3' end of a recovered single-stranded extended second target-specific primer (e.g., after attachment of first universal adapter) can be contacted with a terminal transferase, thereby appending a 3' tail region to the 3' end of the recovered single-stranded extended second target-specific primer and generating a tailed single-stranded extended second target-specific primer. The tailed single-stranded extended second target-specific primer can be contacted with a second universal adapter that is a splint adapter having a double-stranded region and a 3' single-stranded overhang region that is complementary to the 3' tail region of the tailed single-stranded extended second target-specific primer, thereby hybridizing the second universal adapter to the tailed single-stranded extended second target-specific primer. The hybridized second universal adapter can be hybridized such that a 5'-terminal phosphate of the adapter is adjacent to, and can be ligated with, a 3'-terminal OH of the tailed single-stranded extended second target-specific primer. Thus, the 5' end of the hybridized second universal adapter can be contacted with a ligase and ligated to the 3' tail region of the tailed single-stranded extended target-specific primer.

In some cases, the 3' tail region contains, or contains at least about, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 consecutive nucleotides of the same sequence. In some cases, the 3' tail region contains from 2 to about 20, from 2 to about 15, from 2 to about 12, from 2 to about 10, or from 2 to about 8 consecutive nucleotides of the same sequence. In some cases, the 3' tail region contains from 3 to about 20, from 3 to about 15, from 3 to about 12, from 3 to about 10, or from 3 to about 8 consecutive nucleotides of the same sequence.

First, second, or first and second universal adapters can be attached by tagmentation. Methods and compositions for tagmentation include, but are not limited to those described in U.S. Pat. Nos. 5,965,443; 6,437,109; 7,083,980; 7,608,434; and 9,238,671. In an exemplary embodiment, a second double-stranded product is contacted with a transposase

(e.g., a Tn5 transposase or mutant thereof) loaded with first and second adapters, or a pool of first adapter-loaded transposase and second adapter-loaded transposase. The adapter-loaded transposase or pool of adapter-loaded transposases is allowed to fragment the second double-stranded product and covalently link first or second adapters to the end of the fragments, resulting in a pool of: i) fragments having first adapters on both ends; ii) fragments having second adapters on both ends; iii) fragments having a first adapter on a first end and a second adapter on a second end.

Adapter-attached second double-stranded product, recovered single-stranded extended second target-specific primer, or tagmentation fragments thereof, can contain a first universal primer binding site and a second universal primer binding site or complement thereof. Thus, the adapter-attached polynucleotide can be amplified by universal PCR. In one embodiment, a single-stranded polynucleotide (e.g., recovered single-stranded extended second target-specific primer) contains one universal primer binding site at a 3' end and a complement of a different universal primer binding site at the 5' end. In such embodiments, a universal primer can be hybridized to the universal primer binding site and extended with a polymerase, thereby producing a double-stranded product having both first and second universal primer binding sites. In some embodiments, the single-stranded polynucleotide has a second universal primer binding site at a 3' end (e.g., attached by ligation of second universal adapter) and a complement of a first universal primer binding site at a 5' end (e.g., attached by ligation of first universal adapter).

d. Barcoding Original Target Polynucleotide

Described above are methods of UD-PETE in which a barcoded (e.g., UID barcoded) second target-specific primer is hybridized to target polynucleotide, extended, and the extension product recovered. In such embodiments, the barcode is incorporated into the extended second target-specific primer. Thus, polymerase errors that are introduced during the extension of second target-specific primer cannot be distinguished from true variants in the sample from which the target polynucleotide is provided. Described herein are methods of UD-PETE in which a barcoded (e.g., UID barcoded) second target-specific primer is used to attach a barcode (e.g., UID barcode) directly to the original target polynucleotide. Thus, polymerase errors are not introduced into the target polynucleotide sequence.

The methods described herein can include preliminary steps of first target-specific hybridization, extension, and second target-specific hybridization as described above. Moreover, the methods described herein can include subsequent steps of universal adapter attachment (e.g., ligation, tagmentation, etc.) as described above.

In some embodiments, the barcoded (e.g., UID barcoded) second target-specific primer is hybridized to target polynucleotide and extended to produce a second double-stranded product wherein the target polynucleotide in the second double-stranded product contains a 3' single-stranded overhang region having a length of at least 1 nucleotide. Alternatively, the barcoded (e.g., UID barcoded) second target-specific primer can be hybridized to target polynucleotide and extended to produce a second double-stranded product wherein the target polynucleotide in the second double-stranded product does not have a 3' single-stranded overhang region. For example, the barcoded (e.g., UID barcoded) second target-specific primer can hybridize to the target polynucleotide such that the 3' terminal nucleotide of the target polynucleotide is hybridized to a nucleotide

of the 3' hybridizing region (e.g., the 5'-terminal nucleotide of the 3' hybridizing region) of the second target-specific primer.

In embodiments wherein the target polynucleotide in the second double-stranded product contains a 3' single-stranded overhang region having a length of at least 1 nucleotide, the 3' single-stranded overhang region can be contacted with a 3'-5' single-stranded DNA exonuclease to remove the overhang region. For example, the 3' single-stranded overhang region can be contacted with Exo I to digest the overhang region. As another example, the 3' single-stranded overhang region can be contacted with T4 polymerase to digest the overhang region.

Second double-stranded product wherein the target polynucleotide in the second double-stranded product does not have a 3' single-stranded overhang region (e.g., after digestion with a 3'-5' single-stranded DNA exonuclease) can then be contacted with a DNA polymerase to extend the 3' end of the original target polynucleotide. The extension reaction can be templated by the 5' overhang region of the extended second target-specific primer. Thus, if the second target-specific primer is barcoded (e.g., UID barcoded) the extension can attach the barcode (i.e., a complement of the barcode sequence of the second target-specific primer) to a 3' end of the original template strand. Similarly, if the second target-specific primer contains a [SPLINT] region, the extension can attach a [SPLINT] region (i.e., a complement of the [SPLINT] region of the second target-specific primer) to a 3' end of the original template strand. In some cases, the extension incorporates a barcode and a [SPLINT] region to a 3' end of the original template strand. In some cases, the extension incorporates from 5' to 3' a barcode and a [SPLINT] region into a 3' end of the original template strand.

In some embodiments, a first universal adapter is attached to the second double-stranded product before digestion of the 3' single-stranded overhang region, if present. In other embodiments, a first universal adapter is attached to the second double-stranded product after digestion of the 3' single-stranded overhang region, if present. In some cases, a first universal adapter is attached to the second double-stranded product after incorporation of a barcode (e.g., UID barcode), a [SPLINT] region, or a barcode and [SPLINT] region by polymerase-mediated extension of the 3' end of the target polynucleotide in the second double-stranded product. In some cases, a first universal adapter is attached to the second double-stranded product before incorporation of a barcode (e.g., UID barcode), a [SPLINT] region, or a barcode and [SPLINT] region by polymerase-mediated extension of the 3' end of the target polynucleotide in the second double-stranded product.

In an exemplary embodiment, a first universal adapter (e.g., double-stranded first universal adapter) is attached (e.g., ligated) to an end of the second double-stranded product that contains the 3' end of the extended second target-specific primer and the 5' end of the target polynucleotide. In some cases, a double-stranded first universal adapter having a blunt end is ligated to the end of the second double-stranded product that contains the 3' end of the extended second target-specific primer in a blunt end ligation reaction. Alternatively, a double-stranded first universal adapter having a cohesive end (i.e., complementary single-stranded overhang) can be ligated to a compatible cohesive end of the second double-stranded product that contains the 3' end of the extended second target-specific primer in a cohesive-end ligation reaction.

For example, in some cases, the 3' end of the extended second target-specific primer contains one, at least one, two, or at least two consecutive adenine nucleotides and the double-stranded first universal adapter contains one, at least one, two, or at least two consecutive thymine nucleotides for T-A ligation to the end of the second double-stranded product. In some cases, a DNA polymerase is selected for second target-specific primer extension to preferentially produce either blunt or cohesive ends and a corresponding blunt or cohesive end first universal adapter is used. Ligation can be performed by contacting the first universal adapter and second double-stranded product with a ligase (e.g., T4 DNA ligase).

A first universal adapter and a second universal adapter are typically attached (e.g., ligated) to opposite ends of the second double-stranded product. In some cases, the first and second universal adapter are attached before extension of the 3' end of the target polynucleotide in the second double-stranded product. In some cases, the first universal adapter is attached before the extension and the second universal adapter is attached after the extension. In some cases, the first universal adapter is attached to the end of the second double-stranded product containing the 3' end of the extended second target-specific primer, and the second universal adapter is attached to the end of the second double-stranded product containing the 5' end of the extended second-target specific primer. Alternatively, the first universal adapter is attached to the end of the second double-stranded product containing the 5' end of the extended second target-specific primer, and the second universal adapter is attached to the end of the second double-stranded product containing the 3' end of the extended second-target specific primer.

In some embodiments, the second target-specific primer contains a UID barcode and [SPLINT] region and a universal adapter containing an MID barcode and universal primer binding site is attached (e.g., ligated) to the 5' end of the extended second target-specific primer in the second double-stranded product. In such cases, attachment of the MID barcoded universal adapter before extension of the 3' end of the target polynucleotide can incorporate the universal primer site and MID barcode into the original target polynucleotide. In some cases, the MID barcoded universal adapter is attached first, and a different universal adapter is attached to the other end of the second double-stranded product second. However, the relative order in which universal adapters are attached to opposite ends of second-double stranded product is interchangeable for different workflows.

e. Recovering Original Target Polynucleotide

In some embodiments, after first and second adapter are ligated, original single-stranded target polynucleotide is recovered. In some cases, the recovered original single-stranded target polynucleotide is barcoded. The recovered barcoded original single-stranded target polynucleotide can contain a UID, an MID, or a UID and an MID. In an exemplary embodiment, the recovered barcoded original single-stranded target polynucleotide contains from 5' to 3': a second universal primer binding site or complement thereof, an original target polynucleotide region that contains consecutive nucleotides from the original target polynucleotide molecule, a UID barcode, an MID barcode, and a first universal primer binding site or complement thereof.

In some embodiments, the barcoded original single-stranded target polynucleotide is recovered from the second double-stranded product by 5' to 3' double-stranded exonuclease digestion (e.g., digestion of the double-stranded prod-

uct with an exonuclease enzyme that degrades a single strand of a double-stranded DNA substrate to produce a single-stranded product). In such embodiments, the universal adapter attached to the end of the second double-stranded product containing the 3' end of the extended second target-specific primer can be blocked at a 5' end such that the 5' end of the adapter-attached original target polynucleotide is blocked from 5' to 3' double-stranded exonuclease digestion. Alternatively, the universal adapter attached to the end of the second double-stranded product containing the 3' end of the extended second target-specific primer can be labeled (e.g., at a 5' end) with an affinity ligand (e.g., biotin) such that the second double-stranded product containing adapter-attached original target polynucleotide can be captured and the copied strand eluted away, e.g., by heating. As yet another alternative, the universal adapter attached to the end of the second double-stranded product containing the 5' end of the extended second target-specific primer can be labeled (e.g., at a 5' end) with an affinity ligand (e.g., biotin) such that the second double-stranded product containing adapter-attached original target polynucleotide can be captured and the original template strand eluted away, e.g., by heating or chemical elution (e.g., by contacting with an acid, or base, or nucleophile to disrupt the affinity between ligand and capture agent or cleave a link between affinity ligand and nucleic acid), and recovered.

In some embodiments, the barcoded original single-stranded target polynucleotide is recovered from the second double-stranded product through the use of endonucleases. Specifically, endonucleases are used to degrade the second primer extension product without degrading the original strand. Certain endonucleases are known to cleave the nucleic acid backbone (phosphodiester bonds) at specific sites. For example, *E. coli* endonuclease VIII cleaves at abasic sites while *E. coli* endonuclease V cleaves at deoxyinosine sites. In some embodiments, the non-conventional base introduces an abasic site that can be specifically cleaved without cleaving DNA in the same reaction. Exemplary enzymes that cleave abasic sites include, e.g., Tth Endonuclease IV, Endonuclease IV or Endonuclease VIII. In some embodiments, the non-conventional base that introduces the abasic site is Int 1',2'-Dideoxyribose. In some embodiments, one or both of first and second primer extension reactions are performed in the presence of non-conventional nucleotides that can be incorporated by the extending DNA polymerase and enable subsequent endonuclease digestion. In some embodiments, the extension reaction is performed in the presence of deoxyuracil triphosphate (dUTP). In some embodiments, dUTP is entirely replacing dTTP in the extension reaction. In other embodiments, a mixture of dUTP and dTTP is used. The ratio of dUTP to dTTP can be between 0:1, 1:1, 1:100. Following the incorporation of dU in place of some or all dT nucleotides in one or both of first and second primer extension products enables them to be digested with uracil-N-DNA glycosylase (UNG). UNG cleaves the uracil from DNA leaving an abasic site. In some embodiments, the reaction mixture comprising one or both of first and second primer extension products with abasic sites can be treated with an endonuclease cleaving DNA at abasic sites. In some embodiments, the endonuclease is *E. coli* endonuclease VIII. In some embodiments, one or both of first and second primer extension products with abasic sites can be cleaved non-enzymatically, e.g., by heat treatment. In some embodiments, the efficiency of the heat cleavage can be increased by the addition of polyamine compounds such as spermidine, spermine, triethylenetetramine, and trimethylenediamine, see U.S. Pat. No. 8,669,

061. In other embodiments, the extension reaction is performed in the presence of deoxyinosine triphosphate (dITP). Because dITP is incorporated by DNA polymerases opposite any base, dITP in the reaction mixture may partially or completely replace any one of dATP, dCTP, dGTP and dTTP. In some embodiments, dITP is simply added to the mixture of the dATP, dCTP, dGTP and dTTP without reducing the amount of any of the four bases. In some embodiments, the reaction mixture comprising one or both of first and second primer extension products with deoxyinosines (dI) can be treated with an endonuclease cleaving DNA at dI sites. In some embodiments, the endonuclease is *E. coli* endonuclease V. In some embodiments, the DNA fragments resulting from exonuclease digestion are further digested with exonuclease or removed from the reaction mixture by any other means (e.g., size separation).

In some embodiments, the strand paired with the bar-coded original single-stranded target polynucleotide (the second primer extension product) is not removed by endonucleases but is rendered non-amplifiable in the amplification step. In this embodiment, only the primer binding site contains non-conventional nucleotides such as deoxyuracil or deoxyinosine or Int 1',2'-Dideoxyribose. The endonuclease digestion degrades the primer binding site portion of the second primer extension product preventing primer annealing and amplification. In some embodiments, the primer is a universal primer. In this embodiment, an oligonucleotide containing the primer binding site is synthesized by any method known in the art that allows non-conventional nucleotides such as deoxyuracil (dU) or deoxyinosine (dI) or Int 1',2'-Dideoxyribose to be incorporated. In the embodiment where dU is incorporated, the reaction mixture is contacted with uracil-N-DNA glycosylase (UNG). UNG cleaves the uracil from DNA leaving an abasic site. The sample is further contacted with an endonuclease cleaving the DNA at abasic sites. In some embodiments, the endonuclease is *E. coli* endonuclease VIII. Following the endonuclease digestion, the primer binding site no longer supports primer binding and extension.

In the embodiment where dI is incorporated, the reaction mixture is contacted with an endonuclease such as *E. coli* endonuclease V. Following the endonuclease digestion, the primer binding site no longer supports primer binding and extension.

f. UD-PETE for Library Construction and Analysis

Described herein are unidirectional double-primer extension target enrichment (UD-PETE) methods for enriching a plurality of structurally different target polynucleotides from a sample. The enriched target polynucleotides can be a library for downstream analysis (e.g., a high-throughput sequencing library). In some embodiments, the plurality of structurally different target polynucleotides includes target polynucleotides encoding, or encoding at least, 100; 1,000; 5,000; 15,000; 20,000; 30,000; 40,000; 50,000; 100,000; 250,000; 500,000; or 1,000,000 different target sequences. In some cases, at least some proportion of the different target sequences overlap by at least 1 nucleotide but do not overlap by all nucleotides.

The plurality of structurally different target polynucleotides can, e.g., be or include a panel of target polynucleotides that are implicated in, or useful for, diagnosis or monitoring of cancer. As another example, the plurality of structurally different target polynucleotides can, e.g., be or include a panel of target polynucleotides that are implicated in, or useful for, diagnosis or monitoring of an autoimmune disease, such as multiple sclerosis or systemic lupus erythematosus. As yet another example, the plurality of structur-

ally different target polynucleotides can, e.g., be subset, or all, or substantially all (e.g., >90%), immune receptor targets (e.g., B cell receptors (BCRs), T cell receptors (TCRs), γ/δ TCRs, α/β TCRs, TCR β -chains, TCR δ -chains, TCR α -chains, TCR γ -chains, BCR heavy chains, BCR light chains, BCR κ -chains, BCR λ -chains, or a combination or subset of a combination of one or more thereof). In some cases, the plurality of structurally different target polynucleotides can be all or substantially all (e.g., >90%), exomes in a genomic sample. In some cases, the combination of structurally different target polynucleotides encode all or substantially all (e.g., >90%) of the genomic sequence in a sample. In some cases, the combination of structurally different target polynucleotides encode a fraction (e.g., about or at least about 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, or 45%), a substantial fraction (e.g., about or at least about 50%, 75%, or 90%), or substantially all (e.g., at least 95%, 99%, 99.9%, or 99.99%), of the mRNA sequences in the sample.

Generally, the methods involve performing one or more of the foregoing first target-specific primer hybridization and extension reactions in a reaction mixture (e.g., in a single reaction mixture) using a plurality of structurally different first target-specific primers that hybridize to a plurality of structurally different target polynucleotides to thereby generate a plurality of extended first target-specific primers. In some cases, single stranded target or non-target polynucleotides, or both, in a reaction mixture are removed using one or more of the methods described herein. For example, the removing can include single-stranded exonuclease digestion. Additionally or alternatively, the removing can include immobilization of double-stranded products containing an affinity liganded (e.g., biotinylated) first target-specific primer extension product and washing away of non-immobilized polynucleotides. In some cases, the first target-specific primer is immobilized because it is covalently attached to a solid surface (e.g., before or after hybridization to target polynucleotide or before or after extension of the first target specific primer that is hybridized to the target polynucleotide). In such cases, the double-stranded products containing the immobilized first target-specific primer can be washed to remove non-immobilized polynucleotides. Methods and compositions for covalently attaching a target-specific primer to a solid surface are well known in the art and include, but are not limited to, those utilizing N-Hydroxysuccinimide-, epoxy-, or aldehyde-based chemistries. In some cases, the removing also removes un-extended first target-specific primers (e.g., single-stranded exonuclease digestion).

Similarly, the method can further include performing one or more of the foregoing second target-specific primer hybridization and extension reactions (e.g., in a single reaction mixture) using a plurality of structurally different second target-specific primers that hybridize to the plurality of structurally different target polynucleotides to thereby generate a plurality of extended second target-specific primers.

In some embodiments, the method can include trimming 3' overhang regions of the plurality of structurally different hybridized target polynucleotides produced by second target-specific primer extension as described herein (e.g., with a 3' to 5' single stranded DNA exonuclease). Alternatively, the method can include hybridizing the second target-specific primers such that the 3' overhang regions of the plurality of structurally different hybridized target polynucleotides are absent (i.e., the 3' terminal nucleotide of the target polynucleotide is hybridized to the second target-

specific primer). In such embodiments, the method can include extending a 3' end of the hybridized target polynucleotide (e.g., a trimmed 3' end), thereby incorporating additional 5' sequence of the second-primer extension product (e.g., a barcode such as a UID barcode) as described herein. In some cases, the extending the 3' end of the hybridized target polynucleotide is performed after attachment (e.g., ligation) of a first or a first and second adapter, thus incorporating an adapter sequence including, but not limited to, a universal primer binding sequence, a barcode (e.g., an MID barcode), or the combination thereof.

In some embodiments, the plurality of structurally different target polynucleotides having one or more incorporated barcodes, one or more universal primer binding sites, or a combination thereof, can be recovered from double-stranded products containing such. Methods for recovering such target polynucleotides are described above. In some cases, the target polynucleotides are recovered by 5' to 3' double-stranded DNA exonuclease digestion of 5' blocked target polynucleotides (e.g., target polynucleotides attached at the 5' end to a 5' blocked universal adapter). In some cases, the target polynucleotides are recovered by immobilization of affinity ligand labeled (e.g., biotinylated) target polynucleotide (e.g., target polynucleotides attached at the 5' end to an affinity ligand labeled universal adapter) or otherwise immobilized target polynucleotide and washing away, melting away, or melting and washing away, of hybridized second target-specific primer extension product. In some cases, the target polynucleotides are recovered by immobilization of affinity ligand labeled (e.g., biotinylated) second target-specific primer extension product (e.g., second target-specific primer extension products attached at the 5' end to an affinity ligand labeled universal adapter) or otherwise immobilized target polynucleotide, washing away, melting away, or melting and washing away, of hybridized target polynucleotide, and recovering single-stranded target polynucleotide in solution. In some cases, the immobilized target polynucleotide is attached at the 5' end to a universal adapter that is covalently attached to a solid surface (e.g., via N-Hydroxysuccinimide-, aldehyde-, or epoxy-based chemistry).

In some embodiments, double-stranded products containing first target-specific primers and/or second target-specific primers that are hybridized to target polynucleotides are recovered. For example, the double-stranded products can be immobilized by immobilization of labeled second target-specific primer extension product that is hybridized to target polynucleotide. In some cases, the labeled second target-specific primer extension product is a second target-specific primer extension product attached at the 5' end to a labeled universal adapter, wherein the label is an affinity ligand (e.g., biotin) or label suitable for covalent attachment to a solid surface. The immobilized double-stranded product can then be washed and eluted. For example, a covalent attachment between the label and solid surface can be cleaved to elute the double-stranded product.

In some embodiments, the method includes attaching (e.g., ligating) a first and second universal adapter (e.g., containing forward and reverse universal primer binding sites respectively) to opposite ends of a plurality of structurally different double-stranded products generated by the second target-specific primer hybridization and extension. In some embodiments, extended second target-specific primers are recovered from the double-stranded products generated by second target-specific primer hybridization and extension as described herein. In such embodiments, the method can further include attaching (e.g., ligating) a first and second

universal adapter (e.g., containing forward and reverse universal primer binding sites respectively) to opposite ends of a plurality of structurally different extended and recovered second target-specific primers.

In some embodiments, a first, second, or first and second universal adapter is attached by splint ligation using an adapter that hybridizes to, e.g., a splint region of a second-target specific primer or a tail region generated by a terminal transferase reaction, as described herein. In some embodiments, a first, second, or first and second universal adapter is attached by tagmentation (e.g., transposase mediated adapter attachment), as described herein.

One or more of the foregoing plurality of i) adapter-attached double-stranded products; ii) adapter-attached second target-specific primer extension products; or iii) adapter-attached target polynucleotides can be amplified by universal amplification (e.g., universal PCR). Adapter-attached double-stranded products that can be amplified by universal amplification include those containing second-primer extension products, those containing a target polynucleotide (e.g., trimmed target polynucleotide, barcoded target polynucleotide (e.g., UID barcoded, MID barcoded, or the combination thereof), or trimmed and barcoded target polynucleotide), or those containing a second target-specific primer extension product hybridized to one of the foregoing target polynucleotides.

Adapter-attached second target-specific primer extension products that can be amplified by universal amplification include, but are not limited to, adapter-attached tailed second target-specific primer extension products, adapter-attached recovered second target-specific primer extension products, or adapter-attached tailed and recovered second target-specific primer extension products, as described herein. Adapter-attached target polynucleotides that can be amplified by universal amplification include, but are not limited to, adapter-attached trimmed target polynucleotide, barcoded target polynucleotide (e.g., UID barcoded, MID barcoded, or the combination thereof), or trimmed and barcoded target polynucleotide, as described herein.

Described herein are methods for analyzing target polynucleotide sequences enriched from a sample. Generally, the methods include performing any one or more of the UD-PETE methods described herein to obtain a sample enriched for a target polynucleotide, plurality of structurally different target polynucleotides, extended second target-specific primers, a plurality of structurally different extended second target-specific primers, or amplification products thereof. In some cases, the enriched polynucleotides, extended primers, or amplification products thereof contain a sequencing platform-specific adapter region at one or both ends that is compatible for sequencing with one or more known high-throughput sequencing platforms (e.g., a sequencing platform from Illumina, Complete Genomics, BGI, 454 Life Sciences, Ion Torrent, Pacific Biosciences, Genia, or Oxford Nanopore). In some cases, the sequencing platform-specific adapter region is attached by attaching first, second, or first and second universal adapter(s) as described above. The enriched polynucleotides, extended primers, or amplification products thereof contain a sequencing platform-specific adapter region at one or both ends that is compatible for sequencing with one or more known high-throughput sequencing platforms can then be sequenced using the appropriate platform and protocols.

UD-PETE methods described herein can provide enrichment of target polynucleotides, copies thereof (e.g., second target-specific primer extension products), or amplification products thereof from a sample, such that high-throughput

sequencing of the enriched sample provides a high number of on-target reads (e.g., a high number of on-target reads in comparison to single-primer PETE, hybrid capture, or multiplex PCR, or a combination thereof). As used herein, “on-target reads” refers to sequence reads of polynucleotides that contain a region that is substantially the same as, or complementary to, the 3' hybridizing region of the second target-specific primers used in the second target-specific primer extension reaction.

In some cases, “on-target reads” additionally or alternatively refers to sequence reads of polynucleotides that contain a region that is substantially the same as, or complementary to, the 3' hybridizing region of the first target-specific primers used in the reaction. Typically, the region is the same as or complementary to a sequence of a polynucleotide that is expected to hybridize to the first, second, or first and second target-specific primer(s) under typical hybridization conditions (e.g., target-specific primer hybridization conditions) used in PETE applications. Such hybridization conditions can include, but are not limited to, hybridization in isothermal amplification buffer (20 mM Tris-HCl, 10 mM (NH₄)₂SO₄, 50 mM KCl, 2 mM MgSO₄, 0.1% TWEEN® 20, pH 8.8 at 25° C.) at a temperature of about 40° C., 45° C., 50° C., 55° C., 60° C., 65° C., or 70° C.

In some cases, the on-target reads produced by high-throughput sequencing of a sample generated by one or more of the methods described herein can be at least, or at least about, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or higher.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, one of skill in the art will appreciate that certain changes and modifications may be practiced within the scope of the appended claims. In addition, each reference provided herein is incorporated by reference in its entirety to the same extent as if each reference was individually incorporated by reference. Where a conflict exists between the instant application and a reference provided herein, the instant application shall dominate.

EXAMPLES

Example 1. Removal of the Second Primer Extension Product from the Original Strand

In this example, the steps of hybridizing and extending a first target-specific primer to form a first double-stranded product, removing single-stranded target and non-target polynucleotides that are not hybridized to extended target-specific primer, hybridizing and extending a second target-specific primer to form a second double-stranded product comprising a barcode are performed as described generally herein, except that the second primer extension product has been synthesized in the presence of deoxyuracil and a mixture of UNG and endonuclease VIII is used to remove it as described below.

20 µL of the primer extension reaction was mixed with the buffer and the two-enzyme mixture (USER®, New England BioLabs, Mass.) as recommended by the manufacturer and incubated for 10 min at 37 deg. The undegraded DNA (the original strand) was separated from the products of degradation and the reaction mixture using KapaPure SPRI beads (KAPA). The purified DNA was analyzed by qPCR.

FIG. 4 shows PCR Ct (Cq) values from the amplification reaction performed with and without the removal of the

second strand. With the digestion, the total amount of amplifiable strands of DNA is reduced by half (only 1 strand of the 2 in duplex DNA has a uracil incorporated). As expected, the data shows this 50% reduction as a 1 cycle increase in Ct of the PCR.

Example 2

Libraries were prepared from 50 ng Promega Male human genomic DNA, sheared using Covaris E220, and a mix of 117 target specific primers. These libraries were sequenced to determine the success of enrichment of the target regions during the library preparation.

Library preparation commenced with the shearing of high quality DNA using Covaris physical shearing through sonication as shown below.

To physically shear human genomic DNA, a Covaris E220 system was used. The water bath on the instrument is filled to water level 6 and allowed to degas and cool to 7 C. Once complete a maximum of 5 ug and 130 uL of genomic DNA (promega male, Catalog #G152A) in 10 mM Tris-1 mM EDTA, pH 8.0 is loaded into microTUBE AFA Fiber Snap-Cap (PN 520045). The samples are then placed into a Rack 96 Place microTUBE Crimp-Cap (PN 500282). The rack is set to the home position and shearing begins per sizing guidelines provided by Covaris. An Intensifier (PN 500141) was used but Y-dithering was not, per Covaris guidelines. For mean target peak sizing of 300 bp, the following parameters were set: Peak Incident Power (W) is set to 140, Duty Factor is set to 10%, Cycles per Burst is set to 200, and Treatment Time is set to 80 s. Once complete, remove samples from the Covaris E220 and transfer sheared DNA into microcentrifuge tubes.

The fragmented DNA was run on an AGILENT Bioanalyzer to assess shearing success.

Sheared DNA was then used as the input DNA into the Primer 1 Hybridization and Extension Reaction outlined in Table 2.

TABLE 2

Component	uL into Reactions	Final Concentration
DNA	Total 50 ng	1 ng/uL
KAPA 2G Multiplex Mastermix	10	1x
117 Target Specific Biotinylated Primers	1.5	300 nM total, 2.56 nM each
dATP	1.9	3.8 mM
MgCl ₂	5	5 mM
Water	Up to 50 uL	n/a

Samples were then incubated as outlined in Table 3.

TABLE 3

Step	° C.	Time	Ramp Rate
Denaturation	95	5 min	Standard to 80° C.
	80	1 second	0.1-0.3° C./second to 60° C.
Hybridization	60	10 min	Standard to 65° C.
Extension	65	2 min	Standard to 4° C.
	4	HOLD	

Following hybridization and extension with biotinylated primers, samples were mixed at a 1:1 ratio with Dynabeads™ MyOne™ Streptavidin T1 beads. These beads were prepared prior to addition to DNA samples by washing four times with 1× Binding and Wash (B&W) buffer, and resus-

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pending in 2× B&W buffer. The composition of the B&W buffer is described in Table 4.

TABLE 4

Component	Final in 2x Buffer	Final in 1x Buffer
Tris-HCl (pH 7.5)	40 mM	20 mM
EDTA	2 mM	1 mM
NaCl	2M	1M
Tween	0.1%	0.05%
Water	—	—

Samples were incubated with 50 uL MyOne™ beads for 10 minutes at room temperature on a rotor. Once biotinylated DNA had bound to beads, samples were placed on a magnet for 3 minutes and the supernatant was then removed and discarded. Beads were washed with the 1× B&W buffer described in Table 4 four times to remove non-biotinylated DNA. The samples were then washed with 10 mM Tris pH 7.5 to remove excess salts and were then resuspended in 20 uL of 10 mM Tris, pH 7.5.

The resuspended beads were then taken into the Ligation Reaction for ligation of the adaptor sequences to the 3' end of DNA extended in the Primer 1 Hybridization and Extension Reaction. The composition of the Ligation Reaction is described in Table 5.

TABLE 5

Component	uL into Reactions	Final Concentration
DNA + Beads	20	
TA Adaptor	1	20 mM
KAPA Ligation Buffer*	10	1x
KAPA Ligation Enzyme*	5	1x
Water	Up to 50 uL	n/a

*From the KAPA LTP Library Preparation Kit

Ligation Reactions were incubated at 20° C. for 30 minutes.

Following ligation samples were placed on a magnet at room temperature for 1-3 minutes, the supernatant was removed, and samples were washed twice with the 1× B&W buffer described in Table 4.

The samples were then washed with 10 mM Tris pH 8.0 to remove excess salts and were then resuspended in 20 uL of 10 mM Tris, pH 7.5.

These samples were then taken into the Primer 2 Hybridization Reaction outlined in Table 6. During this reaction, target specific primers with outnested portions, equivalent to the sequencing adaptor, are hybridized upstream of the primers added in Primer 1 Hybridization and Extension.

TABLE 6

Component	uL into Reactions	Final Concentration
DNA + Beads	20	
KAPA2G Buffer A	10	1x
117 Outnested Target Specific Primers	1.5	300 nM total, 2.56 nM each
Water	Up to 50 uL	n/a

Primer 2 Hybridization Reactions were incubated at 50° C. for 90 minutes. Samples were then washed as described for the Ligation reactions. Samples were resuspended in 20 uL 10 mM Tris, pH 7.5.

The resuspended beads were then taken into the Extension 2 Reaction. This reaction enabled the extension of Primer 2

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and resulted in the release of target DNA molecules into solution. The composition of the Extension 2 reaction is described in Table 7.

TABLE 7

Component	uL into Reactions	Final Concentration
DNA + Beads	20	
KAPA2G Buffer A	10	1x
dNTPs	1	0.2 mM each
KAPA2G Fast DNA Polymerase	1	5 U
Water	Up to 50 uL	n/a

Extension 2 Reaction samples were incubated at 50° C. for 2 minutes and were then placed directly onto a magnet on ice for 1-3 minutes.

The supernatant (45 uL) was then removed without disturbing the beads, and added to an equal volume (45 uL) of SPRI® beads. A 1× clean-up was performed and samples were eluted in 25 uL 10 mM Tris, pH 7.5.

A qPCR reaction was performed to determine the number of cycles (Ct+5) required to amplify the captured molecules for sequencing. Samples crossed threshold after 24 cycles.

TABLE 8

Component	uL into Reactions	Final Concentration
DNA	2	
KAPA HiFi SybrFast Mix Optimixed for Roche LC480	5	1x
HotStart ReadyMix		
P1 Primer	1.5	750 nM
Indexed Adaptor Primer	1.5	750 nM
Water	Up to 50 uL	n/a

The last step of the library preparation was the Amplification Reaction. This reaction increased the concentration of the samples, completed the sequencing adaptor sequences and added sample indexes. The amplification reaction and cycling parameters are outlined in Tables 9 and 10.

TABLE 9

Component	uL into Reactions	Final Concentration
DNA	20	
KAPA HiFi HotStart ReadyMix	25	1x
P1 Primer	1.25	250 nM
Indexed Adaptor Primer	1.25	250 nM
Water	Up to 50 uL	n/a

TABLE 10

Step	° C.	Time	Cycles
Initial Denaturation	98	1 min	n/a
Denaturation	98	15 sec	26 (10 ng) or 28 (50 ng)
Hybridization	60	30 sec	
Extension	72	30 sec	
Final Extension	72	1 min	n/a
	4	HOLD	n/a

A 1× SPRI® clean-up of the PCR product was then performed and the library was eluted in 25 uL 10 mM Tris, pH 7.5.

Libraries were sequenced on the Illumina MiSeq system using v3 chemistries. Libraries were prepared using standard guidelines for denaturation and dilution.

The sequencing results for 50 ng of Covaris sheared DNA included are On-Target Rate and Coverage Uniformity. See,

FIG. 7A-B. On-Target rate was calculated as the percent of reads with primers were found mapping to the correct location and a number of bases downstream of the primer matching an expected sequence. Coverage uniformity is calculated as a percent of the total probes that fell within a 0.5x and 2x range of the mean coverage uniformity.

The following oligos were used to during the preparation of libraries:

For the Ligation

20170324P5_TA AATGATACGGCGACCACCGAGATCTACACTAGATCGCTCGTCGGCAGCG
[N/S/E]501 TCAGATGTGTATAAGAGACAGT (SEQ ID NO: 1)
20170324P5 C /5Phos/CTGTCTCTTATACACATCTGACGCTGCCGACGA (SEQ ID
TA33 NO: 2)

For qPCR

C5 Universal AATGATACGGCGACCACCGA (SEQ ID NO: 3)
Primer
20170324P7_ CAAGCAGAAGACGGCATAACGAGAT[index]GTCTCGTGGGCTCGGAGA
N70X TGTGTATAAGAGACAG (SEQ ID NO: 4)

For Final Amplification

20170324P7_ CAAGCAGAAGACGGCATAACGAGAT[index]GTCTCGTGGGCTCGGAGA
N70X TGTGTATAAGAGACAG (SEQ ID NO: 5)
C5 Universal AATGATACGGCGACCACCGA (SEQ ID NO: 6)
Primer

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sequence

(SEQ ID NO: 7)
/5Biosg/TGAAAGCTGTACCATACCTGT
(SEQ ID NO: 8) 35
/5Biosg/AGGTTAATATCCGCAAATGACTTG
(SEQ ID NO: 9)
/5Biosg/AGATGATCCGACAAGTGAGAG
(SEQ ID NO: 10) 40
/5Biosg/TACGTCTCCTCCGACCAC
(SEQ ID NO: 11)
/5Biosg/CGCAGCCTGTACCCAGTG
(SEQ ID NO: 12) 45
/5Biosg/GCGGAAGATGAAGATTTCCGGAT
(SEQ ID NO: 13)
/5Biosg/GTTAGCTCATTTTTGTTAATGGTGG
(SEQ ID NO: 14) 50
/5Biosg/TTAAACTTTTCTTTTAGTTGTGCTGA
(SEQ ID NO: 15)
/5Biosg/GTATGCAACATTTCTAAAGTTACCTAC
(SEQ ID NO: 16) 55
/5Biosg/AAGACCATAACCCACCACAG
(SEQ ID NO: 17)
/5Biosg/CTGGAAGGGACGAACTGGT
(SEQ ID NO: 18) 60
/5Biosg/CGACCCAGTTACCATAGCAA
(SEQ ID NO: 19)
/5Biosg/AGAAAATGGAAGTCTATGTGATCAAG
(SEQ ID NO: 20)
/5Biosg/CATTTTAAATTTCTTTCTTAGGTGAAG 65

-continued

(SEQ ID NO: 21)
/5Biosg/GGTCTTGGCCGAGGTCTC
(SEQ ID NO: 22)
/5Biosg/CAGCACCATGGGCACGTC
(SEQ ID NO: 23)
/5Biosg/GAGAGGTGAAAGCGAGAG

-continued

(SEQ ID NO: 24)
/5Biosg/CACTCTTGCCACACCCGC
(SEQ ID NO: 25)
/5Biosg/CTGTATTTATTTTCAAGTGTACTTACCTG
(SEQ ID NO: 26)
/5Biosg/TTATATTCAATTTAAACCCACCTATAATGG
(SEQ ID NO: 27)
/5Biosg/GTATCAAAGAATGGTCTGCAC
(SEQ ID NO: 28)
/5Biosg/ACACAACACAAAATAGCCGTATA
(SEQ ID NO: 29)
/5Biosg/TCTATTCTTTCTTTTGTAGTGTCCA
(SEQ ID NO: 30)
/5Biosg/TGATTTCTGTTTTTACCTCCTAAAGAA
(SEQ ID NO: 31)
/5Biosg/ATCTTTAAAGAGAAATTTGCTAAAGCTGTG
(SEQ ID NO: 32)
/5Biosg/ACGTGTTTTGATCAAAGAAGAGG
(SEQ ID NO: 33)
/5Biosg/AGCCTCACGTTGGTCCAC
(SEQ ID NO: 34)
/5Biosg/GGATGGCTAGGCGAGGAG
(SEQ ID NO: 35)
/5Biosg/AGGGACTAGGCGTGGGAT
(SEQ ID NO: 36)
/5Biosg/CCAAGCCCTAGGGTGGTG
(SEQ ID NO: 37)
/5Biosg/ACGCTCTTCTCACTCATATCC

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-continued

(SEQ ID NO: 38)
/5Biosg/AAGAAATCTTAGACGTAAGCCCCTC

(SEQ ID NO: 39) 5
/5Biosg/TCCCATACCCTCTCAGCG

(SEQ ID NO: 40)
/5Biosg/GGATGAGCTACCTGGAGGAT

(SEQ ID NO: 41) 10
/5Biosg/ATTTTGTAGTGTAGACTGGAAACT

(SEQ ID NO: 42)
/5Biosg/GGGCAGTGCTAGGAAAGAG

(SEQ ID NO: 43) 15
/5Biosg/TGCTTACCTCGCTTAGTGC

(SEQ ID NO: 44)
/5Biosg/GCCGGGATGTGATGAGA

(SEQ ID NO: 45) 20
/5Biosg/CAGGGTCAGAGGCAAGC

(SEQ ID NO: 46)
/5Biosg/AGGGCCACTGACAACCAC

(SEQ ID NO: 47) 25
/5Biosg/TGTTTCTGTCATCCAAATACTCC

(SEQ ID NO: 48)
/5Biosg/AGTGAGGAATCAGAGGCCT

(SEQ ID NO: 49) 30
/5Biosg/GTGCTGTGACTGCTTGTA

(SEQ ID NO: 50)
/5Biosg/ACGGCCAGGCATTGAAGT

(SEQ ID NO: 51)
/5Biosg/AAACCGTAGCTGCCCTGG

(SEQ ID NO: 52) 35
/5Biosg/TCAAATTGCTTCAGAAATTGGAG

(SEQ ID NO: 53)
/5Biosg/ACAAGGTGGAGAGAGTGAAAC

(SEQ ID NO: 54) 40
/5Biosg/GCCATCGTTGTCCACTGAA

(SEQ ID NO: 55)
/5Biosg/TGGTGTTCATTGCTTACTTTG

(SEQ ID NO: 56) 45
/5Biosg/GCAGAGAAGTTATATGCTGAGGAG

(SEQ ID NO: 57)
/5Biosg/CTGCTGCTGGAATTGGTGT

(SEQ ID NO: 58) 50
/5Biosg/TCAAAGAAACACCTTGCTGGA

(SEQ ID NO: 59)
/5Biosg/CACCGCATCGACTCCACC

(SEQ ID NO: 60) 55
/5Biosg/CAGCTGGTTCCGGAAGAAA

(SEQ ID NO: 61)
/5Biosg/TGCAGATTGGGCCTTGGG

(SEQ ID NO: 62) 60
/5Biosg/TGGAAATTTCTGGGCCATGA

(SEQ ID NO: 63)
/5Biosg/ACAGAGAAATGTTGTACAGATTGAG

(SEQ ID NO: 64) 65
/5Biosg/TCAATAGTGCAGATGGGAGG

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(SEQ ID NO: 65)
/5Biosg/GCGGGTCTCTCGGAGGAA

(SEQ ID NO: 66)
/5Biosg/AGAAGCAAGAAAATACCCCCT

(SEQ ID NO: 67)
/5Biosg/CGACTTTGTGACCTTCGGC

(SEQ ID NO: 68)
/5Biosg/CCAATGGACTGTTTTACAATGCC

(SEQ ID NO: 69)
/5Biosg/TTATTTATTTTACAGAGTAACAGACTAGC

(SEQ ID NO: 70)
/5Biosg/CCAAACCTGACCAAACCTGTTCTTATTAC

(SEQ ID NO: 71)
/5Biosg/TGATGCTTGGCTCTGGAAT

(SEQ ID NO: 72)
/5Biosg/CGAAAGACCCTAGCCTTAGAT

(SEQ ID NO: 73)
/5Biosg/GTTTCGTATTTATAGCTGATTTGATGG

(SEQ ID NO: 74)
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(SEQ ID NO: 75)
/5Biosg/TCTGGATCCCACACCTTTAC

(SEQ ID NO: 76)
/5Biosg/GCTATGGCTTTCTAGAAATAGAAAC

(SEQ ID NO: 77)
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(SEQ ID NO: 79)
/5Biosg/GCTGCTCGCAACGTCCTC

(SEQ ID NO: 80)
/5Biosg/CGTTTGGAAAGCTAGTGGTTC

(SEQ ID NO: 81)
/5Biosg/TCTCCAGAGTGCTCTAATGAC

(SEQ ID NO: 82)
/5Biosg/CCATCACCCTTACCTTGTG

(SEQ ID NO: 83)
/5Biosg/CAGAGACTTGGCAGCCAG

(SEQ ID NO: 84)
/5Biosg/AGAAATATCCTCCTTACTCATGGT

(SEQ ID NO: 85)
/5Biosg/GCTTTTACTGATTAACGTAAATACAAGAT

(SEQ ID NO: 86)
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(SEQ ID NO: 87)
/5Biosg/TTCAGCAAATCGAAAAGGACAT

(SEQ ID NO: 88)
/5Biosg/AATTGTTTATCATAACAGACACTTCATTT

(SEQ ID NO: 89)
/5Biosg/TCAACTACCGAATGGACCA

(SEQ ID NO: 90)
/5Biosg/TGAGGAATTTGTCTTGGCGAG

(SEQ ID NO: 91)
/5Biosg/CCAAGGCATCTCATCGTAGTA

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/5Biosg/GTCAGACAATTTTAATACTGGCAAC

(SEQ ID NO: 93) 5
/5Biosg/GTTCTGAAAAGATAGAAGTTTGGAG

(SEQ ID NO: 94)
/5Biosg/TTGCAGATCTCCACCACTG

(SEQ ID NO: 95) 10
/5Biosg/GGTCTACCACTGAATTACATTGTG

(SEQ ID NO: 96)
/5Biosg/CGGAAAATTCAAATAGGACATGTTCTATG

(SEQ ID NO: 97) 15
/5Biosg/GAATGAAAGATGGGCAAGACC

(SEQ ID NO: 98)
/5Biosg/CACATTTTGGACAGCAGGAAT

(SEQ ID NO: 99) 20
/5Biosg/AGGCAGAATCAGCTCCATCC

(SEQ ID NO: 100)
/5Biosg/GACTTATTGTGTAGAAGATACTCCAATA

(SEQ ID NO: 101) 25
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(SEQ ID NO: 102)
/5Biosg/AGCACCTAGAACCAATCC

(SEQ ID NO: 103)
/5Biosg/CGAAATCTCCCTCCAAAAGTG

(SEQ ID NO: 104) 30
/5Biosg/TGAGAGTCGTTTCGATTGCCA

(SEQ ID NO: 105)
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(SEQ ID NO: 106) 35
/5Biosg/TGAAAAGAGAGAGAGTGGACC

(SEQ ID NO: 107)
/5Biosg/ACGGAAAGTACTCCAGATGG

(SEQ ID NO: 108) 40
/5Biosg/GTTCAGGAAAATGACAATGGGA

(SEQ ID NO: 109)
/5Biosg/GTCCTTCTGTAGGCTGGAT

(SEQ ID NO: 110) 45
/5Biosg/CACAAAATGGATCCAGACAACT

(SEQ ID NO: 111)
/5Biosg/AGTTGTTAAACATATCCTATTACTTG

(SEQ ID NO: 112) 50
/5Biosg/GTGAGGGCTGAGGTGACC

(SEQ ID NO: 113)
/5Biosg/GCCAGTTAACGTCTTCCTTCT

(SEQ ID NO: 114) 55
/5Biosg/TTCTGGCCACCATGCGAA

(SEQ ID NO: 115)
/5Biosg/CTCACAGCAGGGTCTTCTC

(SEQ ID NO: 116) 60
/5Biosg/TCAAGATCACAGATTTTGGGC

(SEQ ID NO: 117)
/5Biosg/CACGTGTTGAAGTCTTCGT

(SEQ ID NO: 118) 65
/5Biosg/CTCCGGGCTGAACTTTC

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(SEQ ID NO: 119)
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(SEQ ID NO: 120)
/5Biosg/CGATGGCCAGCTCCTCA

(SEQ ID NO: 121)
/5Biosg/CACGGTTCGGGTGAGAGT

(SEQ ID NO: 122)
/5Biosg/TTTTTCCTTAGTCTTTCTTTGAAGC

(SEQ ID NO: 123)
/5Biosg/TCATATCACTAAGCGCTACTAGA

sequence (SEQ ID NO: 124)
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ACTGATGCAAACCTCTTG (SEQ ID NO: 125)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWAAATAATG

CTCCTAGTACCTGTAGA (SEQ ID NO: 126)
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TACAGAATATGGGTAAAGAT (SEQ ID NO: 127)
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TTGCAGACAAACTC (SEQ ID NO: 128)
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CAGAGCATACTG (SEQ ID NO: 129)
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GTAGCTGAGGG (SEQ ID NO: 130)
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GTTTTTCTTGATAGTATTAATG (SEQ ID NO: 131)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWTCTTCTCT

AAGTGCAAAAGATAACT (SEQ ID NO: 132)
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CTTTTAAATACCTGTTAAGTTT (SEQ ID NO: 133)
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GCACAATATCCTTTT (SEQ ID NO: 134)
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TTCACTGTAAAGC (SEQ ID NO: 135)
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TATATGTTCTTAAATGGCTACG

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(SEQ ID NO: 136)
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 AGAGGAAACCT

(SEQ ID NO: 137)
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 TAAGATGAGTCATATTTGTGG

(SEQ ID NO: 138)
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWCTGTGGGG
 TGGAGAGCTG

(SEQ ID NO: 139)
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(SEQ ID NO: 140)
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 TCTGCTCCCT

(SEQ ID NO: 141)
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 TCAGCGCACT

(SEQ ID NO: 142)
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 TTTGCAGAAAACAGATCT

(SEQ ID NO: 143)
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 TACTCCTTAATGTCACCTAT

(SEQ ID NO: 144)
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 CAGAGAAACCTTTATC

(SEQ ID NO: 145)
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 TTTACCATGATAACG

(SEQ ID NO: 146)
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 CACAAATTTTTAAGGTTACTGA

(SEQ ID NO: 147)
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(SEQ ID NO: 148)
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 AGTGAAGGATATAGGATAC

(SEQ ID NO: 149)
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 TCCTCAGACATTCA

(SEQ ID NO: 150)
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWCCACAGAG
 AAGTTGTTGAGGG

(SEQ ID NO: 151)
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWGCCTTGTA
 CTGCAGAGACAA

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(SEQ ID NO: 152)
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWTACGGGCT
 TGGTCC

(SEQ ID NO: 153)
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWTACAGCGG
 AGAAGGGAGCG

(SEQ ID NO: 154)
 GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWAGGTAGG
 ATCCAGCCCA

(SEQ ID NO: 155)
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 AAGCCAACAA

(SEQ ID NO: 156)
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(SEQ ID NO: 157)
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(SEQ ID NO: 160)
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 TTGTCTGCT

(SEQ ID NO: 161)
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(SEQ ID NO: 162)
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(SEQ ID NO: 163)
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(SEQ ID NO: 166)
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(SEQ ID NO: 167)
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(SEQ ID NO: 168)
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(SEQ ID NO: 170)
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(SEQ ID NO: 171)
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TTTGAGGGACAG

(SEQ ID NO: 172)
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(SEQ ID NO: 173)
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(SEQ ID NO: 174)
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TTAGGTCTGTAC

(SEQ ID NO: 175)
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(SEQ ID NO: 176)
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(SEQ ID NO: 177)
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TGGCGTTTG

(SEQ ID NO: 178)
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(SEQ ID NO: 179)
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(SEQ ID NO: 180)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWTGTTTTG
AACTGTCGATTTTTCAAT

(SEQ ID NO: 181)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWTTGACCAT
GACCATGTAAACG

(SEQ ID NO: 182)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWTCTCACTC
ACCGGGCGAG

(SEQ ID NO: 183)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWCTACATTA
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(SEQ ID NO: 184)
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(SEQ ID NO: 185)
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ATTCTCAACTGCC

(SEQ ID NO: 186)
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(SEQ ID NO: 187)
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(SEQ ID NO: 188)
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(SEQ ID NO: 189)
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(SEQ ID NO: 190)
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(SEQ ID NO: 191)
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TTATCTGAGTAAAACAAC

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(SEQ ID NO: 193)
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(SEQ ID NO: 195)
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CCGTGATCTG

(SEQ ID NO: 197)
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CATCTGGGCCAC

(SEQ ID NO: 198)
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(SEQ ID NO: 199)
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CACCACCAGCA

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(SEQ ID NO: 200)
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(SEQ ID NO: 201)
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(SEQ ID NO: 209)
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GACATGATGATAATAGG

(SEQ ID NO: 210)
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(SEQ ID NO: 211)
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(SEQ ID NO: 212)
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TACCTCTCAGGAAG

(SEQ ID NO: 213)
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TACAATTTCACTAAGTCG

(SEQ ID NO: 214)
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TCCTTCACAGAA

(SEQ ID NO: 215)
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(SEQ ID NO: 216)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWCACACCTT
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(SEQ ID NO: 217)
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(SEQ ID NO: 218)
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(SEQ ID NO: 219)
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CAGCAGTGTCAC

(SEQ ID NO: 220)
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(SEQ ID NO: 222)
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(SEQ ID NO: 223)
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(SEQ ID NO: 224)
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(SEQ ID NO: 225)
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CCTCCACA

(SEQ ID NO: 226)
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CACGGTAATAATTT

(SEQ ID NO: 227)
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GCCTCAATTCTTACCATC

(SEQ ID NO: 228)
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(SEQ ID NO: 229)
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CTGCTTTCCA

(SEQ ID NO: 230)
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ATCTCACAATTG

(SEQ ID NO: 231)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWGGTCCATG
TGCCCCCTCCT

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(SEQ ID NO: 232)
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TGATGATCTGTCC

(SEQ ID NO: 233)
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CACCGCAGCATG

(SEQ ID NO: 234)
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AGTTGGGAGCG

(SEQ ID NO: 235)
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GGAGACTGGT

(SEQ ID NO: 236)
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GCGGCATCTA

(SEQ ID NO: 237)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWCAGGTACC

GTGCGACATC

(SEQ ID NO: 238)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWCAGCGTGT

CCAGGAAGCC

(SEQ ID NO: 239)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWACAAACAG

TCAAACAACAATTCTTTGTAC

(SEQ ID NO: 240)
GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGWNNNNNNWTGACTCCA

CGAGAACTTGATC

Example 3: 9-Target Panel

Libraries were prepared from 10 and 50 ng Promega Male Human Genomic DNA, sheared using KAPA Frag, and a mix of 9 target specific primers. These libraries were sequenced on the Illumina Miseq to assess the success of enrichment of the target regions during the library preparation.

An AGILENT Bioanalyzer trace of the final libraries was prepared. FIG. 8A-B shows the high level sequencing results of the libraries; namely on target rate and genome equivalent recovery (GER) (A), as well as probe coverage uniformity (B). On-Target rate was calculated as the percent of reads with primers were found mapping to the correct location and a number of bases downstream of the primer matching an expected sequence. Coverage uniformity was calculated as a percent of the total probes that fell within a 0.5x and 2x range of the mean coverage uniformity. Libraries prepared with 10 and 50 ng input DNA performed similarly with regards to on-target rate (58-64%), GER (~12%) and uniformity (0.89-1).

Library preparation commenced with the shearing of high quality DNA using KAPA Frag (KAPA Biosystems) as shown in Table 11.

TABLE 11

Component	uL into Reactions	Final Concentration
DNA	Total of 200 ng	4 ng/uL
KAPA Frag Buffer	5	1x
KAPA Frag Enzyme	10	1x
Water	Up to 50 uL	n/a

Samples were vortexed briefly, spun down and incubated at 37° C. for 15 minutes. After incubation, 5 uL of KAPA Frag Stop Solution was added to the reactions. Thereafter 165 uL of SPRI® beads were used to clean up the reactions. DNA was eluted in 20 uL 10 mM Tris-Cl, pH 8.0 for a final concentration of 10 ng/uL. The fragmented DNA was run on an AGILENT Bioanalyzer to assess shearing success.

Sheared DNA was then used as the input DNA into the Primer 1 Hybridization and Extension Reaction outlined in Table 12.

TABLE 12

Component	uL into Reactions	Final Concentration
DNA	Total of 10 or 50 ng	0.2 or 1 ng/uL
KAPA 2G Custom Mastermix	10	1x
9 Target Specific Biotinylated Primers	1.5	30 nM total, 3.3 nM each
dATP	1.9	3.8 mM
MgCl ₂	5	5 mM
Water	Up to 50 uL	n/a

Samples were then incubated as outlined in Table 13

TABLE 13

Step	° C.	Time	Ramp Rate
Denaturation	95	5 min	Standard to 80° C.
	80	1 second	0.1-0.3° C./second to 60° C.
Hybridization	60	10 min	Standard to 65° C.
	65	2 min	Standard to 4° C.
Extension	4	HOLD	

Following hybridization and extension with biotinylated primers, samples were mixed at a 1:1 ratio with Dynabeads™ MyOne™ Streptavidin T1 beads. These beads were prepared prior to addition to DNA samples by washing four times with 1x Binding and Wash (B&W) buffer, and resuspending in 2x B&W buffer. The composition of the B&W buffer is described in Table 14.

TABLE 14

Component	Final in 2x Buffer	Final in 1x Buffer
Tris-Cl—HCl (pH 7.5)	40 mM	20 mM
EDTA	2 mM	1 mM
NaCl	2M	1M
Tween	0.1%	0.05%
Water	—	—

Samples were incubated with 50 uL MyOne™ beads for 10 minutes at room temperature on a rotor. Once biotinylated DNA had bound to beads, samples were placed on a magnet for 3 minutes and the supernatant was then removed and discarded. Beads were washed with the 1x B&W buffer described in Table 14 four times to remove non-biotinylated DNA, and were then resuspended in 20 uL of 10 mM Tris-Cl, pH 8.0.

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The resuspended beads were then taken into the Ligation Reaction for ligation of the adaptor sequences to the 3' end of DNA extended in the Primer 1 Hybridization and Extension Reaction. The composition of the Ligation Reaction is described in Table 15.

TABLE 15

Component	uL into Reactions	Final Concentration
DNA + Beads	20	
TA Adaptor	2	20 mM
KAPA Ligation Buffer*	10	1x
KAPA Ligation Enzyme*	5	1x
Water	Up to 50 uL	n/a

*From the KAPA LTP Library Preparation Kit

Ligation Reactions were incubated at 20° C. for 30 minutes.

Following ligation samples were placed on a magnet at room temperature for 1-3 minutes, the supernatant was removed, and samples were washed twice with the 1x B&W buffer described in Table 14.

Samples were then resuspended in 20 uL 10 mM Tris-Cl, pH 8.0.

These samples were then taken into the Primer 2 Hybridization Reaction outlined in Table 16. During this reaction, target specific primers with outneste portions, equivalent to the sequencing adaptor, are hybridized upstream of the primers added in Primer 1 Hybridization and Extension.

TABLE 16

Component	uL into Reactions	Final Concentration
DNA + Beads	20	
KAPA2G Buffer A	10	1x
9 Outneste Target Specific Primers	1.5	30 nM total, 3.3 nM each
Water	Up to 50 uL	n/a

Primer 2 Hybridization Reactions were incubated at 50° C. for 10 minutes.

Samples were then washed as described for the Ligation reactions.

Samples were resuspended in 20 uL 10 mM Tris-Cl, pH 8.0.

The resuspended beads were then taken into the Extension 2 Reaction. This reaction enabled the extension of Primer 2 and resulted in the release of target DNA molecules into solution. The composition of the Extension 2 reaction is described in Table 17.

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TABLE 17

Component	uL into Reactions	Final Concentration
DNA + Beads	20	
5 KAPA2G Buffer A	10	1x
dNTPs	1	0.2 mM each
KAPA2G Fast DNA Polymerase	1	5 U
Water	Up to 50 uL	n/a

10 Extension 2 Reaction samples were incubated at 50° C. for 2 minutes and were then placed directly onto a magnet on ice for 1-3 minutes.

15 The supernatant (45 uL) was then removed without disturbing the beads, and added to an equal volume (45 uL) of SPRI® beads. A 1x clean-up was performed and samples were eluted in 25 uL 10 mM Tris-Cl, pH 8.0.

20 A qPCR reaction was performed to determine the number of cycles (Ct+2) required to amplify the captured molecules for sequencing. FIG. 9 shows the Cts obtained for each sample.

25 The last step of the library preparation was the Amplification Reaction. This reaction increased the concentration of the samples, completed the sequencing adaptor sequences and added sample indexes. The amplification reaction and cycling parameters are outlined in Tables 18 and 19.

TABLE 18

Component	uL into Reactions	Final Concentration
DNA	20	
KAPA HiFi HotStart ReadyMix	25	1x
P1 Primer	1.25	250 nM
Indexed Adaptor Primer	1.25	250 nM
Water	Up to 50 uL	n/a

TABLE 19

Step	° C.	Time	Cycles
40 Initial Denaturation	98	1 min	n/a
Denaturation	98	15 sec	26 (10 ng) or 28 (50 ng)
Hybridization	60	30 sec	
Extension	72	30 sec	
Final Extension	72	1 min	n/a
45	4	HOLD	n/a

A 1x SPRI® clean up of the PCR product was then performed and the library was eluted in 25 uL 10 mM Tris-Cl, pH 8.0.

TABLE 20

Name	Biotinylated Target Specific Sequence (Inner Primer)
chr9 - 21970722_Bio	/5Biosg//iSp18//iSp18//iSp18/ GGGACGGCCTGAGTCTCC (SEQ ID NO: 241)
chr14 + 105246626_Bio	/5Biosg//iSp18//iSp18//iSp18/ CTGGGTGTGCCAGGACAG (SEQ ID NO: 242)
chr18 + 48591980_Bio	/5Biosg//iSp18//iSp18//iSp18/ TTGATTGTATAGTCAGATAGTTACTTTAAAAAATT (SEQ ID NO: 243)
chr18 - 48604592_Bio	/5Biosg//iSp18//iSp18//iSp18/ GCAGCAGCTGACAGACCTAA (SEQ ID NO: 244)
chr18 + 48604706_Bio	/5Biosg//iSp18//iSp18//iSp18/ GGACCGGATTACCCAAGACAG (SEQ ID NO: 245)

TABLE 20-continued

Name	Biotinylated Target Specific Sequence (Inner Primer)
chr18 - 48591738_Bio	/5Biosg//iSp18//iSp18//iSp18/ GGAAATAAATGGGAAAGAACATCCTCC (SEQ ID NO: 246)
chr13 - 48919139_Bio	/5Biosg//iSp18//iSp18//iSp18/ AATCAGTAACCTTAAAAATTTGTGTTATTTTCG (SEQ ID NO: 247)
chr18 - 48573338_Bio	/5Biosg//iSp18//iSp18//iSp18/ ATGTCTCCAATTTCTGAAGCAATTTTG (SEQ ID NO: 248)
chr18 + 48573611_Bio	/5Biosg//iSp18//iSp18//iSp18/ AGCTCATCCTAGTAAATGTGTTACCATAC (SEQ ID NO: 249)

The adaptors used in the ligation reaction were prepared from the oligonucleotides listed in Table 21.

TABLE 21

Name	Sequence
160201P5_W	AATGATACGGCGACCACCGAGATCTACACTCTTT CCCTACACGACGCTCTTCCGATCT (SEQ ID NO: 250)
160201P5_C_ TA19	/5phos/GATCGGAAGAGCGTCGTGT (SEQ ID NO: 251)

The primers used in Primer 2 Hybridization are listed in Table 22.

TABLE 22

Name	Outnested Target Specific Sequence (Outer Primer)
Ochr9 - 21970772n	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT WNNNNNWCTCAGCGCCAATCGGT (SEQ ID NO: 252)
Ochr14 + 105246608n	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT WNNNNNWAGGCAGCCAGGCAGGAA (SEQ ID NO: 253)
Ochr18 + 48591955n	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT WNNNNNWAGAAGCCATTGAGAGAGCAAGTA (SEQ ID NO: 254)
Ochr18 - 48604642n	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT WNNNNNWCGAAGGTCATCAACCAATTCCA (SEQ ID NO: 255)
Ochr18 + 48604681n	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT WNNNNNWAGGATGAGTTTTGTGAAAGGCTGG (SEQ ID NO: 256)
Ochr18 - 48591788n	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT WNNNNNWGGAACACCAATACTCAGGAGCTATA (SEQ ID NO: 257)
Ochr13 - 48919189n	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT WNNNNNWATGGACTACAAAGGAAAGAATAGA AAAAAGTA (SEQ ID NO: 258)
Ochr18 - 48573388n	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT WNNNNNWGTCCATTTGTTCAAGTTTTTCTTTTA AATCAAAT (SEQ ID NO: 259)

TABLE 22-continued

Name	Outnested Target Specific Sequence (Outer Primer)
Ochr18+ 48573575n	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT WNNNNNWTTGGATCTTTAATAACAGCTATAACT ACAAATGG (SEQ ID NO: 260)

The primers used in the qPCR reaction are listed in Table 23.

TABLE 23

Name	Outnested Target Specific Sequence (Outer Primer)
OUnivAmp	GTGACTGGAGTTCAGACGTGTG (SEQ ID NO: 261)
P1	AATGATACGGCGACCACCGA (SEQ ID NO: 6)

The primers used in the Amplification Reaction are listed in Table 24.

TABLE 24

Name	Outnested Target Specific Sequence (Outer Primer)
D70X	CAAGCAGAAGACGGCATAACGAGAT[index]GTGACTGGAGTT CAGACGTGTGCTCTTC (SEQ ID NO: 262)
P1	AATGATACGGCGACCACCGA (SEQ ID NO: 6)

Example 4:117-Target Panel with KAPA Frag DNA

Libraries were prepared from 10 ng Coriell (NA12878) DNA, sheared using KAPA Frag as described in Example 3, and a mix of 117 target specific primers at 3.4 or 34 nM each in the Primer 1 Hybridization and Extension Reaction. These libraries were sequenced on the Illumina Nextseq (Mid Output 300x).

A LabChip GX trace of the final libraries was prepared. FIG. 10A-B show the high level sequencing results of the libraries calculated as described in Example 3; namely on target rate and genome equivalent recovery (GER) (FIG.

10A), as well as probe coverage uniformity (FIG. 10B). Libraries prepared with 3.4 and 34 nM primer in Primer 1 Hybridization and Extension Reaction performed similarly, although some differences were observed. The on-target rates are slightly higher for the 3.4 nM samples (48.5 as opposed to 33.1%), whereas the genome equivalent recovery (GER) and coverage uniformity were slightly higher for the 34 nM samples (4.6 compared to 3.5%, and 0.83 compared to 0.77 respectively).

The first step of library preparation was the Primer 1 Hybridization and Extension Reaction outlined in Table 25.

TABLE 25

Component	uL into Reactions	Final Concentration
DNA	10 ng	0.2 ng/uL
KAPA2G Fast Multiplex PCR	25	1x
117 Target Specific Biotinylated Primers	2	0.4 uM total, 3.4 nM each or 4 uM Total, 34 nM each
dATP	1.9	3.8 mM
MgCl ₂	5	5 mM
Water	Up to 50 uL	n/a

Samples were then incubated as outlined in Table 13.

Following hybridization and extension with biotinylated primers, samples were mixed at a 1:1 ratio with Dynabeads™ MyOne™ Streptavidin T1 beads. These beads were prepared prior to addition to DNA samples by washing four times with 1x Binding and Wash (B&W) buffer, and resuspending in 2x B&W buffer. The composition of the B&W buffer is described in Table 4 with the exception that Tris-Cl pH 7.8 was used instead of Tris-Cl at pH 7.5.

Samples were incubated with 50 uL MyOne™ beads, and bead washes and resuspension were performed as described in Example 1.

The resuspended beads were then taken into the Ligation Reaction as described in Example 3. In this instance, indexed TA adaptors were used.

Following ligation, samples were placed on a magnet at room temperature for 1 minute. The supernatant was removed, and samples were washed with the 1x B&W buffer and eluted in 10 mM Tris-Cl, as described in Example 3.

These samples were then taken into the Primer 2 Hybridization Reaction outlined in Table 26. During this reaction, target specific primers with outnested portions, equivalent to the sequencing adaptor, were hybridized upstream of the primers added in Primer 1 Hybridization and Extension.

TABLE 26

Component	uL into Reactions	Final Concentration
DNA + Beads	20	
KAPA2G Buffer A	10	1x
117 Outnested Target Specific Primers	2	400 nM total, 3.4 nM each
Water	Up to 50 uL	n/a

Primer 2 Hybridization Reactions were incubated at 50° C. for 90 minutes.

Samples were then washed as described for the Ligation reactions.

Samples were resuspended in 20 uL 10 mM Tris-Cl, pH 8.0.

The resuspended beads were then taken into the Extension 2 Reaction as described in Example 3, and outlined in Table

17. This reaction enabled the extension of Primer 2 and resulted in the release of target DNA molecules into solution.

Extension 2 Reaction samples were incubated at 50° C. for 2 minutes and were then placed directly onto a magnet on ice for 1-3 minutes.

The supernatant (47 uL) was then removed without disturbing the beads, and added to an equal volume (47 uL) of SPRI® beads. A 1x clean-up was performed and samples were eluted in 20 uL 10 mM Tris-Cl, pH 8.0.

The final step of the library preparation was the Amplification Reaction outlined in Example 3, with the exception that a 62° C. annealing temperature was used. The amplification reaction and cycling parameters are outlined in Tables 18 and 19.

A 1x SPRI® clean up of the PCR product was then performed and the library was eluted in 25 uL 10 mM Tris-Cl, pH 8.0.

Example 5:117-Target Panel with Tagmented DNA

Six replicate libraries were prepared from 10 ng tagmented Coriell (NA12878) DNA and a mix of 117 target specific primers at 3.4 nM each in the Primer 1 Hybridization and Extension Reaction. These libraries were sequenced on the Illumina Nextseq (Mid Output 300x). A LabChip GX trace of a subset of the final libraries was prepared. FIG. 11A-B show the high level sequencing results of the libraries calculated as described in Example 1; namely on target rate and genome equivalent recovery (GER) (FIG. 11A), as well as probe coverage uniformity (FIG. 11B). Libraries prepared with tagmented DNA did not perform as well as those reported in Examples 3 and 4. The on-target rates were low, with a mean of 3.7%, and the genome equivalent recovery (GER) was less than 1%. The coverage uniformity was also slightly lower than observed in Examples 3 and 4, at ~60%.

To prepare these libraries, DNA was tagmented by incubating DNA with transposomes pre-loaded with partial adaptor sequences (R1 arms), as outlined in Table 27.

TABLE 27

Component	uL into Reactions	Final Concentration
DNA		0.2 ng/uL
Reaction buffer	10	1x
MnCl ₂	2	2 mM
Transposase (0.18 mg/ml)	4	7.2 ng/uL
Water	Up to 20 uL	n/a

The tagmentation reaction was carried out by incubating samples at 55° C. for 5 minutes.

After incubation, samples were incubated at room temperature for 5 minutes with 20 uL of GHCl stop solution.

The samples then underwent a 1x SPRI® clean up and were eluted in 10 uL 10 mM Tris-Cl, pH 8.0.

The eluate was incubated at 95° C. for 5 minutes to denature DNA fragments, thereby ensuring that fragments carried the partial adaptor sequences only on the 5' end.

This DNA was used as the input into the Primer 1 Hybridization and Extension Reaction described in Example 4.

All subsequent library preparation steps were as described in Example 4, with the exception of the Ligation Reaction which was excluded, and the final PCR reaction which made use of different primers.

The ligation reaction was unnecessary since the fragments already had partial adaptor sequences added during fragmentation.

The components of the final PCR reaction are outlined in Table 28.

TABLE 28

Component	uL into Reactions	Final Concentration
DNA	20	
KAPA HiFi HotStart ReadyMix	25	1x
Indexed i5 Adaptor Primer	1.25	250 nM

TABLE 28-continued

Component	uL into Reactions	Final Concentration
Indexed i7 Adaptor Primer	1.25	250 nM
Water	Up to 50 uL	n/a

Post-amplification clean-up were as described in Examples 3-4.

While the invention has been described in detail with reference to specific examples, it will be apparent to one skilled in the art that various modifications can be made within the scope of this invention. Thus the scope of the invention should not be limited by the examples described herein, but by the claims presented below.

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 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 28

 acacaacaca aaatagccgt ata 23

<210> SEQ ID NO 29
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 <212> TYPE: DNA
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 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 29

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tctattcttt cctttgtagt gtcca

25

<210> SEQ ID NO 30
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 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 30

tgattttctgt ttttacctcc taaagaa

27

<210> SEQ ID NO 31
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 31

atctttaaag agaaatttgc taaagctgtg

30

<210> SEQ ID NO 32
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 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 32

acgtgttttg atcaaagaag agg

23

<210> SEQ ID NO 33
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 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 33

agcctcacgt tggteccac

18

<210> SEQ ID NO 34
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 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 34

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ggatggctag gcgaggag 18

<210> SEQ ID NO 35
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <220> FEATURE:
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 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)
 <400> SEQUENCE: 35

agggactagg cgtgggat 18

<210> SEQ ID NO 36
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 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)
 <400> SEQUENCE: 36

ccaagcccta gggtggtg 18

<210> SEQ ID NO 37
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 <212> TYPE: DNA
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 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)
 <400> SEQUENCE: 37

acgctcttct cactcatatc c 21

<210> SEQ ID NO 38
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 <212> TYPE: DNA
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 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)
 <400> SEQUENCE: 38

aagaaatctt agacgtaagc ccctc 25

<210> SEQ ID NO 39
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 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

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<400> SEQUENCE: 39

tcccataccc tctcagcg 18

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 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 40

ggatgagcta cctggaggat 20

<210> SEQ ID NO 41
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 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 41

atthtgagtg ttagactgga aact 24

<210> SEQ ID NO 42
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 42

gggcagtgct aggaagag 19

<210> SEQ ID NO 43
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 43

tgettacctc gcttagtgc 19

<210> SEQ ID NO 44
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

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<400> SEQUENCE: 44
gccgggatg tgatgaga 18

<210> SEQ ID NO 45
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 45
caggggtcag aggcaagc 18

<210> SEQ ID NO 46
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 46
agggccactg acaaccac 18

<210> SEQ ID NO 47
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 47
tgtttctgtc atccaaatac tcc 23

<210> SEQ ID NO 48
<211> LENGTH: 19
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 48
agtgaggaat cagaggcct 19

<210> SEQ ID NO 49
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)

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<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 49

gtgctgtgac tgctttaga 20

<210> SEQ ID NO 50
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 50

acggccaggc attgaagt 18

<210> SEQ ID NO 51
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 51

aaaccgtagc tgccttgg 18

<210> SEQ ID NO 52
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 52

tcaaaattgc ttcagaaatt ggag 24

<210> SEQ ID NO 53
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 53

acaaggtgga gagagtgaaa c 21

<210> SEQ ID NO 54
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base

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<222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 54
 gccatcgttg tccactgaa 19

<210> SEQ ID NO 55
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 55
 tgggtgtcca ttgcttactt tg 22

<210> SEQ ID NO 56
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 56
 gcagagaagt tatatgctga ggag 24

<210> SEQ ID NO 57
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 57
 ctgctgctgg aattggtgt 19

<210> SEQ ID NO 58
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 58
 tcaaagaaac accttgctgg a 21

<210> SEQ ID NO 59
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:

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<221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 59

 caccgcatcg actccacc 18

<210> SEQ ID NO 60
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 60

 cagctggttc cggaagaaa 19

<210> SEQ ID NO 61
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 61

 tgcagattgg gccttggg 18

<210> SEQ ID NO 62
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 62

 tggaaatttc tgggcatga 20

<210> SEQ ID NO 63
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 63

 acagagaaat gttgtacaga ttgag 25

<210> SEQ ID NO 64
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct

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<220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 64

 tcaatagtgc agatgggagg 20

 <210> SEQ ID NO 65
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 65

 gcgggtctct cggaggaa 18

 <210> SEQ ID NO 66
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 66

 agaagcaaga aaataccccc t 21

 <210> SEQ ID NO 67
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 67

 cgactttgtg accttcggc 19

 <210> SEQ ID NO 68
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 68

 ccaatggact gttttacaat gcc 23

 <210> SEQ ID NO 69
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

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<223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 69

 ttatatttatt ttacagagta acagactagc 30

 <210> SEQ ID NO 70
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 70

 ccaaactgac caaactgttc ttattac 27

 <210> SEQ ID NO 71
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 71

 tgatgcttgg ctctggaat 19

 <210> SEQ ID NO 72
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
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 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 72

 cgaaagaccc tagccttaga t 21

 <210> SEQ ID NO 73
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 73

 gtttcgtatt tatagctgat ttgatgg 27

 <210> SEQ ID NO 74
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 74

 ccttatgatt catcaggaga gcatttaa 28

 <210> SEQ ID NO 75
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 75

 tctggatccc acacctttac 20

 <210> SEQ ID NO 76
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 76

 gctatggctt tcctagaata gaaac 25

 <210> SEQ ID NO 77
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 77

 tttttcatga agatgcatac aacg 24

 <210> SEQ ID NO 78
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 78

 gaagaatgta attgataatc tttaccttt 30

 <210> SEQ ID NO 79
 <211> LENGTH: 18
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 79

 gctgctcgca acgtcctc 18

 <210> SEQ ID NO 80
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 80

 cgtttgaaa gctagtggtt c 21

 <210> SEQ ID NO 81
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 81

 tctccagagt gctctaata c 21

 <210> SEQ ID NO 82
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 82

 ccatcaccac ttaccttggt g 21

 <210> SEQ ID NO 83
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 83

 cagagacttg gcagccag 18

 <210> SEQ ID NO 84
 <211> LENGTH: 24

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<212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 84

 agaaatatcc tccttactca tgggt 24

 <210> SEQ ID NO 85
 <211> LENGTH: 29
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 85

 gcttttactg attaacgtaa atacaagat 29

 <210> SEQ ID NO 86
 <211> LENGTH: 26
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 86

 cttttaagtg gtagccatag tatgat 26

 <210> SEQ ID NO 87
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 87

 ttcagcaaat cgaaaaggac at 22

 <210> SEQ ID NO 88
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 88

 aattgtttat catacagaca cttcattt 28

 <210> SEQ ID NO 89

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<211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 89

 tcaactacac gaatggacca 20

<210> SEQ ID NO 90
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 90

 tgaggaatth gtcttgcca g 21

<210> SEQ ID NO 91
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 91

 ccaaggcatc tcatcgtag a 21

<210> SEQ ID NO 92
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 92

 gtcagacaat ttaatactg gcaac 25

<210> SEQ ID NO 93
 <211> LENGTH: 26
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 93

 gttctgaaaa agatagaagt ttggag 26

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<210> SEQ ID NO 94
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
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 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 94

 ttgcagatct ccaccactg 19

<210> SEQ ID NO 95
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 95

 ggtctaccac tgaattacat tgtg 24

<210> SEQ ID NO 96
 <211> LENGTH: 29
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
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 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 96

 cggaaaattc aaataggaca tgttctatg 29

<210> SEQ ID NO 97
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 97

 gaatgaaaga tgggcaagac c 21

<210> SEQ ID NO 98
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 98

 cacattttgg acagcaggaa t 21

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<210> SEQ ID NO 99
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 99

 aggcagaatc agctccatcc 20

<210> SEQ ID NO 100
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 100

 gacttattgt gtagaagata ctccaata 28

<210> SEQ ID NO 101
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 101

 tcagacgaca caggaagc 18

<210> SEQ ID NO 102
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 102

 agcaccctag aaccaaattcc 20

<210> SEQ ID NO 103
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 103

 cgaaatctcc ctccaaaagt g 21

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<210> SEQ ID NO 104
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 104

 tgagagtcgt tcgattgccca 20

<210> SEQ ID NO 105
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 105

 gacaaacat gccaccaag 19

<210> SEQ ID NO 106
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 106

 tgaaaagaga gagagtggac c 21

<210> SEQ ID NO 107
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 107

 acggaaagta ctccagatgg 20

<210> SEQ ID NO 108
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 108

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 gttcaggaaa atgacaatgg ga 22

<210> SEQ ID NO 109
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 109

gtcctttctg taggctggat 20

<210> SEQ ID NO 110
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 110

cacaaaatgg atccagacaa ct 22

<210> SEQ ID NO 111
 <211> LENGTH: 29
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 111

agttgttaaa catatcctat tatgacttg 29

<210> SEQ ID NO 112
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 112

gtgagggctg aggtgacc 18

<210> SEQ ID NO 113
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

 <400> SEQUENCE: 113

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gccagttaac gtcttccttc t 21

<210> SEQ ID NO 114
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 114

ttctggccac catgcgaa 18

<210> SEQ ID NO 115
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 115

ctcacagcag ggtcttctc 19

<210> SEQ ID NO 116
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 116

tcaagatcac agattttggg c 21

<210> SEQ ID NO 117
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 117

cacgtggtga agtcctcgt 19

<210> SEQ ID NO 118
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification (5Biosg)

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<400> SEQUENCE: 118

ctccccgggct gaactttc

18

<210> SEQ ID NO 119

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (1)..(1)

<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 119

tgcgggcatg gttactgc

18

<210> SEQ ID NO 120

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (1)..(1)

<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 120

cgatggccca gctcctca

18

<210> SEQ ID NO 121

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (1)..(1)

<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 121

cacgggtcgg gtgagagt

18

<210> SEQ ID NO 122

<211> LENGTH: 26

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (1)..(1)

<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

<400> SEQUENCE: 122

ttttttcctt agtctttctt tgaagc

26

<210> SEQ ID NO 123

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (1)..(1)

<223> OTHER INFORMATION: 5' biotin modification (5Biosg)

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<400> SEQUENCE: 123

tcatattcac taagegctac taga 24

<210> SEQ ID NO 124

<211> LENGTH: 67

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 124

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgtaaataca actgatgcaa 60

actcttg 67

<210> SEQ ID NO 125

<211> LENGTH: 67

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 125

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwaataatg ctctagtagc 60

ctgtaga 67

<210> SEQ ID NO 126

<211> LENGTH: 70

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 126

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtccttaa tacagaatat 60

gggtaaagat 70

<210> SEQ ID NO 127

<211> LENGTH: 64

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 127

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgtaaacc ttgcagacaa 60

actc 64

<210> SEQ ID NO 128

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<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 128

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gtctcgtggg ctcgagatg tgtataagag acagwnnnnn nwccatgagg cagagcatac    60
g                                                                    61

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<210> SEQ ID NO 129
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 129

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gtctcgtggg ctcgagatg tgtataagag acagwnnnnn nwacatcctg gtagctgagg    60
g                                                                    61

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<210> SEQ ID NO 130
<211> LENGTH: 72
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 130

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gtctcgtggg ctcgagatg tgtataagag acagwnnnnn nwgtcttttg gtttttcttg    60
atagtattaa tg                                                         72

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<210> SEQ ID NO 131
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 131

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gtctcgtggg ctcgagatg tgtataagag acagwnnnnn nwtcttctct aagtgcaaaa    60
gataact                                                                67

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<210> SEQ ID NO 132
<211> LENGTH: 72
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 132

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcagtgttt cttttaaata 60

 cctgttaagt tt 72

 <210> SEQ ID NO 133
 <211> LENGTH: 64
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 133

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwccacagtt gcacaatattc 60

 cttt 64

 <210> SEQ ID NO 134
 <211> LENGTH: 63
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 134

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgcagcaa ttcactgtaa 60

 agc 63

 <210> SEQ ID NO 135
 <211> LENGTH: 72
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 135

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwctaatgta tatatgttct 60

 taaatggcta cg 72

 <210> SEQ ID NO 136
 <211> LENGTH: 61
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 136

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwccaggacc agaggaaacc 60

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t 61

<210> SEQ ID NO 137
 <211> LENGTH: 71
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 137

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwaatagtt taagatgagt 60

catattgtg g 71

<210> SEQ ID NO 138
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 138

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwctgtgggg tggagagctg 60

<210> SEQ ID NO 139
 <211> LENGTH: 61
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 139

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwggtcacac ttgttcccca 60

c 61

<210> SEQ ID NO 140
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 140

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwccgtttga tctgctcct 60

<210> SEQ ID NO 141
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature

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<222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 141

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwctggatgg tcagcgact 60

 <210> SEQ ID NO 142
 <211> LENGTH: 68
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 142

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgttatgat tttgcagaaa 60

 acagatct 68

 <210> SEQ ID NO 143
 <211> LENGTH: 71
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 143

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwactataat tactccttaa 60

 tgtcagctta t 71

 <210> SEQ ID NO 144
 <211> LENGTH: 68
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 144

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgaaaatg gtcagagaaa 60

 cctttatc 68

 <210> SEQ ID NO 145
 <211> LENGTH: 65
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 145

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgcagttg tttaccatga 60

 taacg 65

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<210> SEQ ID NO 146
 <211> LENGTH: 72
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 146
 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcgaaataa cacaaatddd 60
 taaggttact ga 72

<210> SEQ ID NO 147
 <211> LENGTH: 65
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 147
 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgattaca cagtatcctc 60
 gacat 65

<210> SEQ ID NO 148
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 148
 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwctgaaaag agtgaaggat 60
 ataggatac 69

<210> SEQ ID NO 149
 <211> LENGTH: 64
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 149
 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwactgttct tcctcagaca 60
 ttca 64

<210> SEQ ID NO 150
 <211> LENGTH: 63
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct

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<220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 150

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwccacagag aagttgttga 60

 ggg 63

 <210> SEQ ID NO 151
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 151

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgcccttga ctgcagagac 60

 aa 62

 <210> SEQ ID NO 152
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 152

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtggtgatg ggcttgggtcc 60

 <210> SEQ ID NO 153
 <211> LENGTH: 61
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 153

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtacagcgg agaagggagc 60

 g 61

 <210> SEQ ID NO 154
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 154

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcaggtagg atccagccca 60

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<210> SEQ ID NO 155
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 155

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwatcccca aagccaaca 60

<210> SEQ ID NO 156
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 156

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwggttgggg gtgtgtggtc 60

<210> SEQ ID NO 157
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 157

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwggtgcttc ccattccagg 60

<210> SEQ ID NO 158
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 158

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwacagtcaa gaagaaaacg 60

gc 62

<210> SEQ ID NO 159
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 159

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gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwagaggagc tgggtgtggt 60

g 61

<210> SEQ ID NO 160
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 160

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwaccgcttc ttgtcctgct 60

<210> SEQ ID NO 161
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 161

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgagcagta aggagattcc 60

cc 62

<210> SEQ ID NO 162
 <211> LENGTH: 61
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 162

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwaaatcggg aagagggtggg 60

c 61

<210> SEQ ID NO 163
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 163

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwccccctac tgctcacctg 60

<210> SEQ ID NO 164
 <211> LENGTH: 63
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

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<223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 164

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwccaccaca ctatgtcgaa 60
 aag 63

 <210> SEQ ID NO 165
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 165

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgccagac ctaagagcaa 60
 tc 62

 <210> SEQ ID NO 166
 <211> LENGTH: 61
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 166

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgccacaca acctccgtca 60
 t 61

 <210> SEQ ID NO 167
 <211> LENGTH: 63
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 167

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwacaaaaga aatgcagggg 60
 gat 63

 <210> SEQ ID NO 168
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 168

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gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgcaagaag cccagacgga 60

<210> SEQ ID NO 169
 <211> LENGTH: 65
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 169

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtttcactg tttccaaagg 60

atcaa 65

<210> SEQ ID NO 170
 <211> LENGTH: 64
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 170

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgcatagt ttgatgtgcc 60

atag 64

<210> SEQ ID NO 171
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 171

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgcatgac tttgagggac 60

ag 62

<210> SEQ ID NO 172
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 172

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcatttatt tcctatagct 60

cctgagtat 69

<210> SEQ ID NO 173
 <211> LENGTH: 64
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 173

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgttactt cttggcactt 60
 tagc 64

 <210> SEQ ID NO 174
 <211> LENGTH: 64
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 174

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcttttctg ttaggtctgt 60
 cagc 64

 <210> SEQ ID NO 175
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 175

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwggtattacc caagacagag 60
 ca 62

 <210> SEQ ID NO 176
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 176

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwggtatgg acacgttcat 60
 cc 62

 <210> SEQ ID NO 177
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

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<400> SEQUENCE: 177

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwactgcttc tgggcgtttg 60

<210> SEQ ID NO 178

<211> LENGTH: 60

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 178

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgagccgctc ctgggattgc 60

<210> SEQ ID NO 179

<211> LENGTH: 70

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 179

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwagataaga ataaaacaca 60

tacaagttgg 70

<210> SEQ ID NO 180

<211> LENGTH: 69

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 180

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgtttttg aactgtcgta 60

tttttcaat 69

<210> SEQ ID NO 181

<211> LENGTH: 63

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 181

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwttgacat gaccatgtaa 60

acg 63

<210> SEQ ID NO 182

<211> LENGTH: 60

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T
 <400> SEQUENCE: 182

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtctcactc accgggcgag 60

<210> SEQ ID NO 183
 <211> LENGTH: 72
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 183

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwctacatta ataaccataa 60

agcatgaact at 72

<210> SEQ ID NO 184
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 184

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwggaagaat tttttgatga 60

aacaagacg 69

<210> SEQ ID NO 185
 <211> LENGTH: 63
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 185

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwaagccttt attctcaact 60

gcc 63

<210> SEQ ID NO 186
 <211> LENGTH: 72
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 186

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gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwggaaaaa tatgacaaag 60
aaagctatat aa 72

<210> SEQ ID NO 187
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 187

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcctgaagg tattaacatc 60
atttgctc 68

<210> SEQ ID NO 188
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 188

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwccaatctc tcataaatc 60
ttttctcaat g 71

<210> SEQ ID NO 189
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 189

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwttttgatg acattgcata 60
cattcg 66

<210> SEQ ID NO 190
<211> LENGTH: 72
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 190

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgtaacatt tccaatctac 60
taatgctaat ac 72

<210> SEQ ID NO 191

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<211> LENGTH: 68
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 191

gtctcgtggg ctcgagatg tgtataagag acagwnnnnn nwgacagtga ttatctgagt 60
 aaaacaac 68

<210> SEQ ID NO 192
 <211> LENGTH: 64
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 192

gtctcgtggg ctcgagatg tgtataagag acagwnnnnn nwcgtgtgta gacaggtttc 60
 agtc 64

<210> SEQ ID NO 193
 <211> LENGTH: 65
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 193

gtctcgtggg ctcgagatg tgtataagag acagwnnnnn nwcaccaatt ttaagacaaa 60
 acgct 65

<210> SEQ ID NO 194
 <211> LENGTH: 65
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 194

gtctcgtggg ctcgagatg tgtataagag acagwnnnnn nwccatgaca agattttccc 60
 ttacc 65

<210> SEQ ID NO 195
 <211> LENGTH: 72
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature

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<222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 195

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgttatata ttcaaataac 60

 acccaatgaa ga 72

 <210> SEQ ID NO 196
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 196

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgtgtcca ccgtgatctg 60

 <210> SEQ ID NO 197
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 197

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwactaaact catctggggcc 60

 ac 62

 <210> SEQ ID NO 198
 <211> LENGTH: 71
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 198

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwacctacaa atatttacag 60

 gtaaccattt a 71

 <210> SEQ ID NO 199
 <211> LENGTH: 61
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 199

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwttaattc caccaccagc 60

 a 61

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<210> SEQ ID NO 200
 <211> LENGTH: 67
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 200

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtctcctcc aacctaatag 60

tgtattc 67

<210> SEQ ID NO 201
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 201

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcacagaga cttggcagcc 60

<210> SEQ ID NO 202
 <211> LENGTH: 67
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 202

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwttggttct tatatgcttt 60

tttgctt 67

<210> SEQ ID NO 203
 <211> LENGTH: 66
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 203

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgagaatga tttgacataa 60

ccctga 66

<210> SEQ ID NO 204
 <211> LENGTH: 66
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature

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<222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 204

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwattttagc gaagaatagc 60

 cagaat 66

 <210> SEQ ID NO 205
 <211> LENGTH: 72
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 205

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgaacagt tataatggtc 60

 atacttttat ga 72

 <210> SEQ ID NO 206
 <211> LENGTH: 70
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 206

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwccatctat aatgtgctta 60

 attttttaggg 70

 <210> SEQ ID NO 207
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 207

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgacaggtta ttgcgagtgt 60

 tt 62

 <210> SEQ ID NO 208
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 208

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwttgacaat atagacaatt 60

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 taagtccca 69

<210> SEQ ID NO 209
 <211> LENGTH: 67
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 209

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcaccaatc gacatgatga 60

taatagg 67

<210> SEQ ID NO 210
 <211> LENGTH: 65
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 210

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwagaggaag cttagatagt 60

tctcg 65

<210> SEQ ID NO 211
 <211> LENGTH: 63
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 211

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgaaacttct tcaaagcgag 60

gtt 63

<210> SEQ ID NO 212
 <211> LENGTH: 64
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 212

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgccattca tacctctcag 60

gaag 64

<210> SEQ ID NO 213
 <211> LENGTH: 68
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 213

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcaaacact tacaatttca 60

 ctaagtcg 68

 <210> SEQ ID NO 214
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 214

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwaggcaaag tccttcacag 60

 aa 62

 <210> SEQ ID NO 215
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 215

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcacctcaa gttccaacca 60

 ca 62

 <210> SEQ ID NO 216
 <211> LENGTH: 64
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 216

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcacacctt catctaagtc 60

 caag 64

 <210> SEQ ID NO 217
 <211> LENGTH: 70
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

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<400> SEQUENCE: 217

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcttctatt aaccaagaaa 60
caatacagac 70

<210> SEQ ID NO 218

<211> LENGTH: 69

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 218

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcagctgaa gatgaaatag 60
gatgtaatc 69

<210> SEQ ID NO 219

<211> LENGTH: 62

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 219

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcgaagttc cagcagtgtc 60
ac 62

<210> SEQ ID NO 220

<211> LENGTH: 64

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 220

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtggtgaaat tttcttcagg 60
agcg 64

<210> SEQ ID NO 221

<211> LENGTH: 66

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(41)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 221

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcttctgtc agttcacttg 60
atagtt 66

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<210> SEQ ID NO 222
 <211> LENGTH: 63
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 222
 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgatctt ccagatagcc 60
 ctg 63

<210> SEQ ID NO 223
 <211> LENGTH: 68
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 223
 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwagtaccta aaaataaagc 60
 acctactg 68

<210> SEQ ID NO 224
 <211> LENGTH: 67
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 224
 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgatactt tattacattt 60
 tgccacg 67

<210> SEQ ID NO 225
 <211> LENGTH: 67
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 225
 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwaattaaga ataatgcctc 60
 cagttca 67

<210> SEQ ID NO 226
 <211> LENGTH: 65
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:

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<221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 226

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwatttcagc cacgggtaat 60

 aattt 65

 <210> SEQ ID NO 227
 <211> LENGTH: 68
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 227

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgaaaaata gcctcaattc 60

 ttaccatc 68

 <210> SEQ ID NO 228
 <211> LENGTH: 71
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 228

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgaaacagtg aatatttcct 60

 ttgatgatat t 71

 <210> SEQ ID NO 229
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 229

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgctctggca ctgctttcca 60

 <210> SEQ ID NO 230
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 230

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtggcacc atctcacaat 60

 tg 62

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<210> SEQ ID NO 231
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T
 <400> SEQUENCE: 231

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwggtccatg tgccccctct 60

<210> SEQ ID NO 232
 <211> LENGTH: 63
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T
 <400> SEQUENCE: 232

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtcttccca tgatgatctg 60

tcc 63

<210> SEQ ID NO 233
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T
 <400> SEQUENCE: 233

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwggtgaaaa caccgcagca 60

tg 62

<210> SEQ ID NO 234
 <211> LENGTH: 61
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T
 <400> SEQUENCE: 234

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgtttggtc agttgggagc 60

g 61

<210> SEQ ID NO 235
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 235

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgcaagacc ggagactggt      60

<210> SEQ ID NO 236
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 236

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgaccttcc gcggcatcta      60

<210> SEQ ID NO 237
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 237

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcaggtacc gtgcgacatc      60

<210> SEQ ID NO 238
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 238

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwcagcgtgt ccaggaagcc      60

<210> SEQ ID NO 239
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(41)
<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 239

gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwgacaacag tcaaacaaca      60

attctttgta c                                                                71

<210> SEQ ID NO 240
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(41)
 <223> OTHER INFORMATION: N is A, C, G, or T

 <400> SEQUENCE: 240

 gtctcgtggg ctcggagatg tgtataagag acagwnnnnn nwtgactcca cgagaacttg 60

 atc 63

 <210> SEQ ID NO 241
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification linked to [18-carbon
 spacer (x3)] = /5Biosg//iSp18//iSp18//iSp18/

 <400> SEQUENCE: 241

 gggacggcct gagtctcc 18

 <210> SEQ ID NO 242
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification linked to [18-carbon
 spacer (x3)] = /5Biosg//iSp18//iSp18//iSp18/

 <400> SEQUENCE: 242

 ctgggtgtgc caggacag 18

 <210> SEQ ID NO 243
 <211> LENGTH: 35
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification linked to [18-carbon
 spacer (x3)] = /5Biosg//iSp18//iSp18//iSp18/

 <400> SEQUENCE: 243

 ttgattgtat agtcagatag ttactttaaa aaatt 35

 <210> SEQ ID NO 244
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification linked to [18-carbon
 spacer (x3)] = /5Biosg//iSp18//iSp18//iSp18/

 <400> SEQUENCE: 244

-continued

gcagcagctg acagacctaa

20

<210> SEQ ID NO 245
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification linked to [18-carbon
 spacer (x3)] = /5Biosg//iSp18//iSp18//iSp18/
 <400> SEQUENCE: 245

ggaccggatt acccaagaca g

21

<210> SEQ ID NO 246
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification linked to [18-carbon
 spacer (x3)] = /5Biosg//iSp18//iSp18//iSp18/
 <400> SEQUENCE: 246

ggaaataaat gggaaagaac atcctcc

27

<210> SEQ ID NO 247
 <211> LENGTH: 32
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification linked to [18-carbon
 spacer (x3)] = /5Biosg//iSp18//iSp18//iSp18/
 <400> SEQUENCE: 247

aatcagtaac cttaaaaatt tgtggtattt cg

32

<210> SEQ ID NO 248
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification linked to [18-carbon
 spacer (x3)] = /5Biosg//iSp18//iSp18//iSp18/
 <400> SEQUENCE: 248

atgtctccaa tttctgaagc aattttg

27

<210> SEQ ID NO 249
 <211> LENGTH: 29
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base

-continued

<222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' biotin modification linked to [18-carbon spacer (x3)] = /5Biosg//iSp18//iSp18//iSp18/

<400> SEQUENCE: 249

agctcatcct agtaaattgtg ttaccatac 29

<210> SEQ ID NO 250
 <211> LENGTH: 58
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct

<400> SEQUENCE: 250

aatgatacgg cgaccaccga gatctacact ctttcctac acgacgctct tccgatct 58

<210> SEQ ID NO 251
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: 5' phosphorylation (5Phos)

<400> SEQUENCE: 251

gatcggaga gcgctcgtg 19

<210> SEQ ID NO 252
 <211> LENGTH: 58
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(40)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 252

gtgactggag ttcagacgtg tgctcttccg atctwnnnnn wtcacgcgc caatcggg 58

<210> SEQ ID NO 253
 <211> LENGTH: 58
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(40)
 <223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 253

gtgactggag ttcagacgtg tgctcttccg atctwnnnnn waggcagcca ggcaggaa 58

<210> SEQ ID NO 254
 <211> LENGTH: 65
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic nucleotide construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (36)..(40)
 <223> OTHER INFORMATION: N is A, C, G, or T

-continued

<400> SEQUENCE: 254

gtgactggag ttcagacgtg tgctcttccg atctwnnnnn wagaagccat tgagagagca 60
 aggta 65

<210> SEQ ID NO 255

<211> LENGTH: 65

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(40)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 255

gtgactggag ttcagacgtg tgctcttccg atctwnnnnn wagaaggtca tcaacaccaa 60
 ttcca 65

<210> SEQ ID NO 256

<211> LENGTH: 65

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(40)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 256

gtgactggag ttcagacgtg tgctcttccg atctwnnnnn waggatgagt tttgtgaaag 60
 gctgg 65

<210> SEQ ID NO 257

<211> LENGTH: 66

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(40)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 257

gtgactggag ttcagacgtg tgctcttccg atctwnnnnn wggaacacca atactcagga 60
 gctata 66

<210> SEQ ID NO 258

<211> LENGTH: 76

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic nucleotide construct

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (36)..(40)

<223> OTHER INFORMATION: N is A, C, G, or T

<400> SEQUENCE: 258

gtgactggag ttcagacgtg tgctcttccg atctwnnnnn wtatggacac taaaaggaa 60
 agaatagaaa aaagta 76

-continued

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<210> SEQ ID NO 259
<211> LENGTH: 76
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(40)
<223> OTHER INFORMATION: N is A, C, G, or T

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<400> SEQUENCE: 259

gtgactggag ttcagacgtg tgctcttccg atctwnnnnn wgtccatttg ttcaagtttt      60
tccttttaaa tcaaat                                                         76

```

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<210> SEQ ID NO 260
<211> LENGTH: 76
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(40)
<223> OTHER INFORMATION: N is A, C, G, or T

```

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<400> SEQUENCE: 260

gtgactggag ttcagacgtg tgctcttccg atctwnnnnn wttggattct ttaataacag      60
ctataactac aaatgg                                                         76

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<210> SEQ ID NO 261
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct

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<400> SEQUENCE: 261

gtgactggag ttcagacgtg tg                                                         22

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<210> SEQ ID NO 262
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic nucleotide construct
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (24)..(25)
<223> OTHER INFORMATION: 3' end of position 24 (T) conjugated with index
sequence to 5' end of positin 25 (G)

```

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<400> SEQUENCE: 262

caagcagaag acggcatacg agatgtgact ggagttcaga cgtgtgctct tc                52

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What is claimed is:

1. A method for enriching a target polynucleotide from a sample, the method comprising:

- a) providing a reaction mixture comprising the sample⁶⁰ and a first target-specific primer, wherein the sample comprises single-stranded target polynucleotide having a 3' and a 5' end and non-target polynucleotides;
- b) hybridizing a first target-specific primer to the single-stranded target polynucleotide in the reaction mixture,⁶⁵ wherein the first target-specific primer hybridizes at

least 6 nucleotides from the 3' end of the single-stranded target polynucleotide and comprises an affinity ligand;

- c) extending the hybridized first target-specific primer with a DNA polymerase to form a first double-stranded product comprising the target polynucleotide hybridized to the extended first target-specific primer, wherein the hybridized target polynucleotide comprises a single-stranded overhang region of at least 6 consecutive nucleotides at the 3' end;

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- d) removing single-stranded target and non-target polynucleotides from the reaction mixture by capturing the affinity ligand of the first double-stranded product;
- e) hybridizing a second target-specific primer to the single-stranded overhang region at the 3' end of the hybridized target polynucleotide of the captured first double stranded product,
- wherein the second target-specific primer comprises a 3' hybridizing region and a barcode region; and
- f) extending the hybridized second target-specific primer with a DNA polymerase, wherein the DNA polymerase comprises strand displacement activity, 5'-3' double stranded DNA exonuclease activity, or a combination thereof, thereby displacing or degrading the extended first target-specific primer and forming a second double-stranded product comprising a barcode,
- wherein the second double-stranded product comprises the target polynucleotide hybridized to an extended second target-specific primer, wherein the extended second target-specific primer comprises:
- i) a complement of at least a portion of the target polynucleotide; and,
- ii) a single-stranded 5' overhang region comprising the barcode;

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- g) attaching adaptors to the second double-stranded product to form a barcoded and adapted target polynucleotide; and
- h) amplifying the adapted second double-stranded product including the barcoded target polynucleotide thereby enriching the target polynucleotide.
2. The method of claim 1, further comprising prior to step h), removing the extended second target-specific primer from the second double-stranded product using an endonuclease selected from Tth Endonuclease IV, Endonuclease IV, Endonuclease V, and Endonuclease VIII and Uracil-N-DNA glycosylase.
3. The method of claim 1, wherein attaching adapters in step g) comprises ligating an adapter to one end of the second double-stranded product.
4. The method of claim 1, wherein attaching adapters in step g) comprises ligating adapters to at least one end a single-strand of the second double stranded product by splint ligation.
5. The method of claim 1, wherein adapters in step g) comprise universal primer binding sites and amplification in step h) utilizes universal primers.

* * * * *